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GenCore version 4.5
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OM nucleic – nucleic search, using sw model

January 11, 2002, 12:08:49; Search time 282.09 Seconds Run on:

(without alignments)
2130.783 Million cell updates/sec

US-09-820-005-3_COPY_16200_18853 2654 Perfect score:

1 tgictaggccatagcitggc.....agctacitgggaggctgagg 2654 Scoring table: Sequence:

IDENTITY_NUC Gaport 1.0

351203 seqs, 113238999 residues

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued_Patents_NA:* Database

/cgn2_6/ptodata/2/ina/5A_COMB.seq:*
/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/pcrUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/pcrUS_coMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being prinand is derived by analysis of the total score distribution.

SUMMARIES

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Result	L.	Ouerv				
NO	Score	Match	Match Length DB	DB	QI	Description
	1 204	7.7	2713	7	US-08-916-901-6	Sequence 6, Appli
. •	2 204	7.7	2713	4	US-09-154-602-6	ý
O	3 189.4	7.1	2839	4	US-09-061-702-1	7
ر ن	4 172.2	6.5	31571	Н	US-08-323-443B-1	H
υ	5 172.2	6.5	53526	٣	US-08-658-136-2	7
υ	6 172.2	6.5	53577	٣	US-08-658-136-1	+
	7 169.6		6235	4	US-09-305-384-5	'n
~	169.6		6299	4	US-09-305-384-1	1,
-	9 165.4		6949	Н	US-08-480-784-20	20,
Ä	0 165.4		6929	Н	US-08-483-553-20	20,
H			6929	-4	US-08-487-002-20	20,
H			6949	Н	US-08-483-554B-20	20,
H	3 165.4	6.2	6929	Т	US-08-488-011B-20	20,
Ä		6.2	6929	4	US-08-850-727-20	20,
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Ä	6 165.4	6.2	6929	വ	PCT-US95-10203-20	20,
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7		6.2	7210	ري	PCT-US95-07201-10	10,
7		6.2	22481	Ŋ	PCT-US95-07201-43	43,
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7	3 152.4		11811	4	US-09-078-294-7	7,
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7	5 150.6	5.7	6063	7	US-08-788-279-4	4,
c 5	6 149.4		6929		US-08-480-784-20	20,
o '	7 . 149.4	5.6	6929	-	US-08-483-553-20	20.

Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 11, Appl Sequence 27, Appl Sequence 6, Appli Sequence 1, Appli Sequence 1, Appli Sequence 3, Appli Sequence 3, Appli Sequence 1, Appli	
US-08-487-002-20 US-08-483-554B-20 US-08-488-011B-20 US-08-850-727-20 PCT-US95-10202-20 PCT-US95-10203-20 PCT-US95-10203-20 US-08-138-629-8 US-08-138-629-8 US-08-009-27-11 US-09-009-656-11 PCT-US95-009-656-11 US-09-056-105-27 US-08-370-975B-1 US-08-370-975B-1 US-08-370-975B-1 US-08-975-080-35 US-09-630-706-105	
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ALIGNMENTS

APPLICANT: Hillman, Jennifer L.
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: RAB PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 93174 Porter Dr.
CITY: Palo Alto MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA: ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 35,749
REFERENCE/DOCKET NUMBER: PF-0367 US APPLICATION NUMBER: US/08/916,901 FILING DATE: Filed Herewith PRIOR APPLICATION DATA: APPLICATION NUMBER: Sequence 6, Application US/08916901 Patent No. 5892012 TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555 LENGTH: 2713 base pairs TELEFAX: 415-845-4166 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: TYPE: nucleic acid ; STRANDEDNESS: single ; TOPOLOGY: linear US-08-916-901-6 COMPUTER READABLE FORM: 94304 COUNTRY:

6 Score 204; DB 2; Length 27 Pred. No. 7.9e-32; 0; Mismatches 963; Indels Ouery Match 7.7%; Best Local Similarity 31.3%; Matches 443; Conservative

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94304
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Pred. No. 7.9e-32;
                                                                                                                                                                                                                                                                                                                                                                                       caagcctagaatcccagctacttgggaggctgagg 2654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/154,602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION DATE:
FILING DATE:
ATTORNEY-AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RAB PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/916,901
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; Patent No. 6300472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hillman, Jennifer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: RAB PROJ
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
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Best Local Similarity 31.33
Matches 443; Conservative
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CITY: Palo Alto
STATE: CA
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INFORMATION FOR
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us-09-820-005-3_copy_16200_18853.rni

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1697 AAATTAGCCGGCCGTGGTGGCTCACACCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAG 1756
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                                                                                    677 ICTTCCTGTGTTTTCAAAAAGTTGTTGCTGAAATCCTTGGAATCAAATTAAACAAAGCAG 736
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                   617 GGTTTTGCCAGGAAATGGTTTTAATAGCCACTTTGTTTCAGCCAAGGCAAGAGACTCTG
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                                                      CCATTGTGTTGATAGTTTTGGCTGCCCTTCACCTCTGGGTGTGTCTGAGACTTCTAAGA
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                                                                                                                                 1809 CCCTGTCTCTACTAAAATACAAAAACTAGGCCAGGCGGGGGGGCACGCCTGTAATCTC 1868
gagaaaatcgtaaggggagcagatggttgtcaagagaaataggctgaccatcgaag-gact
                                          1757 GAGAATCACTTGAGGTCAGGAGTTT-----GAGACCAGCCTGGCCAACGTGGTGAAA
                                                                               2440 ggcagaagctttcagaaaaccactggacggctgggcacagtggcttaggcctgtaatccc
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Pred. No. 5.8e-29;
0; Mismatches 296; Indels 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Wang, Xiaodong
APPLICANT: Wang, Xiaodong
TITLE OF INVENTION: DNA FRAGMENTATION FACTOR INVOLVED IN
TITLE OF INVENTION: APOPTOSIS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER: US/09/061,702
                                                                                                                                                                                                                                                                                                                                                         Concurrently Herewith
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: McMillian, Nabeela R.
REGISTRATION NUMBER: P-43,363
REFERENCE/DOCKET NUMBER: UTSD:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512)418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 1, Application US/09061702; Patent No. 6165737
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INFORMATION FOR SEQ ID NO: 1:
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EDNESS: single
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COMPUTER READABLE FORM:
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nes 448; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-061-702-1/c
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1929 atgagaatcgcttgaaccgggggaggcagtgttgcagtgagccgagacggcgccactgca 1988
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APPLICANT: BURN, TIMOTHY C.
APPLICANT: BONNORS, TIMOTHY D.
APPLICANT: CONNORS, TIMOTHY D.
APPLICANT: GERMINO, GREGORY
APPLICANT: GERMINO, GREGORY
APPLICANT: PENG
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
WINMER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
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Patent No. 5654170
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APPLICANT: KLINGE
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E: Darby & Darby PC 805 Third Avenue

ADDRESSEE:

CITY: New York

STATE: NO STREET:

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7619 GGGCCCCGGGGTCTGCGCCTGCTGTCCCTACACTCTCCCACACTCTCCTGTCATTCAGGG 7560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7319 ACAATGGGATGTCGGCTCCAACGACCAATTTACAAGAAACACAAAAGCACACACTCACAGC 7260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7259 ACCACGGAGGTGACACCATGGAGGTGGCACCCCCAAGACACGGGGAGAAATCCAGGCTGC 7200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7559 ATGCAGGTGGGAAAGGGCAAGGCCCCGGGTGCTCCTATATTTACATCAGTGAACCAAGC
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                                                                                                                                                                                                              PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 172.2; DB 1;
Pred. No. 2e-25;
); Mismatches 956;
                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: LUGWIG, S. Peter
REGISTRATION NUMBER: 25,351
REFRENCE/DOCKET NUMBER: 0372,
TELECOMMUNICATION INFORMATION:
TELEPAX: (212) 753-627
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 31571 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
~~MEDITHER: IBM PC COMPALIble
~~MEDITHER: IBM PC COMPALIBLE
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ilarity 31.5%;
Conservative 0
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NAME: Ludwig, S. Peter
                                                                                                                                                                                                                                                                                                                                        FILING DATE: 12-OCT-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA: APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLONE: PKD1 GENOMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 448; Conserv
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ORGANISM: HOM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-323-443B-1
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SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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NAME: LASSEN, ELIZABETH
REFESTRATION NIMBER: 31,845
REFERENCE/DOCKET NUMBER: GEN4-17.8
                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/658,136
                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION TELEPHONE: 508-872-8400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic) US-08-658-136-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 53526 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                           CITY: FRAMINGHAM
STATE: MASSACHUSETTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENZYME C
                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                01701
                                                                                                                                              COUNTRY:
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                                                                                                                                                                   1907 cagetactggggaggetgaggeatgagaategettgaaccggggaggeagatgttgeagt 1966
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2320 atgtgaggacgggggggggggcccttagagataagaga----caatcataagggga 2373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2374 gatatcagagaaaatcgtaaggggagcagatggttgtcaaggagaataggctgaccatcga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2434 aggactggcagaagctttcagaaaacca---ctggacggctgggcacagtggcttaggcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7079 GCTGAGGCGGGAGGATCACGAGGTCAGGAGATCCAGACCATCCTGGCTAACACGGTGAAA
                                                                                                                                                                                                                                                                                                                                                                    ---aaaaaaaaaaaaaaaaaaaaaaagtaacttaggtgcagggtgtcctctgttattcactg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  agaccgtgccccggttatgaggttgtaccagaaagcaagtattcactatgcacactattc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2200 tetttececaaaatgeagaeaegaaggtgeaaagtgaagetgeeagtettgeaaaagatg
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                                                                    1847 nnnnnnnnnnnnnnnnnntaaaaattagetgggegtggtggeatgeateeaatee
                                                                                                                     7019 CCCCGTCTCTAAAAATACAAAATTAGCTGGGCATGGTGGCGGGCA---CCAGTCC
                                                                                                                                                                                            gagccgagacggccactgcactccagcctggactacagagcgagactctatctc----
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                                                                                                 8244 ACCACGGAGGTGACACCATGGAGGTGGCACCCCCAAGACACAGCGAGAAATCCAGGCTGC 8185
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                                                                                                                                                                                                                                                                                                 8424 ACCCAGGTGACCCCCAGCCAGGGTGAGTGGCAACCAGCACCAGAAGTGGCCTTTAGAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 53526
Score 172.2; DB 3;
Pred. No. 2.2e-25;
0; Mismatches 956;
Query Match 6.5%;
Best Local Similarity 31.5%;
Matches 448; Conservative
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POLYCYSTIC KIDNEY DISEASE GENE

LANDES, GREGORY M BURN, TIMOTHY C CONNORS, TIMOTHY D DACKOWSKI, WILLIAM GERMINO, GREGORY QIAN, FENG

APPLICANT: DACKOWSKI APPLICANT: GERMINO, CAPPLICANT: GIAN, FENCTILE OF INVENTION:

Sequence 2, Application US/08658136 Patent No. 6071717

US-08-658-136-2/c

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GENERAL INFORMATION:

APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:

KLINGER, KATHERINE

POLYCYSTIC KIDNEY DISEASE GENE

APPLICANT: QIAN, FENG TITLE OF INVENTION: PO NUMBER OF SEQUENCES: 5 CORRESPONDENCE ADDRESS:

GENZYME CORPORATION

ADDRESSEE:

ONE MOUNTAIN ROAD

CITY: FRAMINGHAM STATE: MASSACHUSETTS

USA

COUNTRY:

01701

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/658,136

GEN4-17.8

APPLICAL.

PILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LASSEN, ELIZABETH
REGISTRATION NUMBER: 31,845
REFERENCE/DOCKET NUMBER: 31,845
REFERENCE/DOCKET NUMBER: GEN4TELECOMMUNICATION INFORMATION:
TELEPHONE: 508-872-8400
"""TERPAX: 508-872-5415

TELEPAX: 508-8/2-341 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 53577 base pairs TYPE: nucleic acid

DNA (genomic)

; MOLECULE TYPE: US-08-658-136-1

single

linear

TOPOLOGY:

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 Score 172.2; DB 3;
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 Query Match
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KLINGER, KATHERINE W
LANDES, GREGORY M
BURN, TIMOTHY C
CONNORS, TIMOTHY D
DACKOWSKI, WILLIAM
GERMINO, GREGORY

GENERAL INFORMATION:
APPLICANT: KINGER
APPLICANT: LANDES,
APPLICANT: BURN, T:
APPLICANT: CONNORS
APPLICANT: DACKOWS
APPLICANT: DACKOWS

Sequence 1, Application US/08658136 Patent No. 6071717

US-08-658-136-1/c ; Sequence 1, Appl

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APPLICANT: Heartlein, Michael W.
APPLICANT: Selden, Richard F
TITLE OF INVENTION: GENOMIC SEQUENCES FOR PROTEIN PRODUCTION AND DELIVERY
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FILE REFERENCE: 07236/017001
CURRENT APPLICATION NUMBER: US/09/305,384
CURRENT FILING DATE: 1999-05-05
EARLIER APPLICATION NUMBER: US 60/084,649
EARLIER FILING DATE: 1998-05-07
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastseQ for Windows Version 3.0
SEQ ID NO 5
                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-305-384-5
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                                                            APPLICANT: Treco, Douglas A.
APPLICANT: Treco, Douglas A.
APPLICANT: Heartlein, Michael W.
APPLICANT: Beatlein, Michael W.
APPLICANT: Selden, Richard F.
TITLE OF INVENTION: GENOMIC SEQUENCES FOR PROTEIN PRODUCTION AND DELIVERY FILE REPERENCE: 07236/0117001
CURRENT APPLICATION NUMBER: US/09/305,384
CURRENT FILING DATE: 1999-05-05
EARLIER PAPLICATION NUMBER: US 60/084,649
EARLIER FILING DATE: 1998-05-07
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 6.4%; Score 169.6; DB 4; Length 6679; Best Local Similarity 54.4%; Pred. No. 5.1e-25; Matches 442; Conservative 0; Mismatches 344; Indels 26;
                              Sequence 1, Application US/09305384 Patent No. 6242218
                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-305-384-1
                                                                                                                                                                                                                                                                                                  SEQ ID NO 1
LENGTH: 6679
          -09-305-384-1
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2563 aacatggtgaaaccccatcttacagaaatataaaaattagccaggcgtggtggcacaa 2622
                                                                                                          APPLICANT: Swenson, Jeff
APPLICANT: Kamb, Alexander
APPLICANT: Kamb, Alexander
APPLICANT: Harbman, Keith D.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Futreal, P. Andrew
APPLICANT: Futreal, P. Andrew
TITLE OF INVENTION: 179-Linked Breast and Ovarian Cancer
TITLE OF INVENTION: 89sceptibility Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSEE: Venable, Baetjer, Howard & Civiletti, LLP : 1201 New York Avenue, N.W., Suite 1000 Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                NAME: Innen, Jeffrey L. REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109347
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/300,266
FILING DATE: 02-5EP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,221
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/348,824
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,104
FILING DATE: 16-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,784
                                                                                                                                                                                                                                                                                                                 ; Sequence 20, Application US/08480784
; Patent No. 5693473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 20:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 24-MAR-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Skolnick, Mark
APPLICANT: Goldgar, David
APPLICANT: Miki, Yoshio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 6769 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 202 TELEPHONE: 202 TELEPHONE: 202-962-8300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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COMPUTER: IB
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Sequence 20, Application US/08483553
Patent No. 5709999
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                                                                                                                                                                                                                                                           1869 aaaaattagetyggegtygtggcatgeatceacaateeeagetaetygggaggetgagge 1928
                                                                                                                                                                                                                                                                                                                               1929 atgagaatcgcttgaaccgggggaggcagatgttgcagtgagccgagacggcgccactgca 1988
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                                                                                                                                                                                Length 6769;
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                                                                                                                                                                                Score 165.4; DB 1; Length (Pred. No. 3.4e-24; O; Mismatches 321; Indels
                                                                                                                                                                                6.2%;
                                      DNA (genomic)
                                                                                                        ORGANISM: Homo sapiens
US-08-480-784-20
                                                                                                                                                                                                   Best Local Similarity 55.8
Matches 464; Conservative
double
                 TOPOLOGY: linear MOLECULE TYPE: DNA
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                                                                    ANTI-SENSE: NO ORIGINAL SOURCE:
 STRANDEDNESS:
                                                     HYPOTHETICAL:
                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                     Breast and Ovarian Cancer
                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP STREET: 1201 New York Avenue, N.W., Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 165.4; DB 1;
Pred. No. 3.4e-24;
0; Mismatches 321;
                                                                                          APPLICANT: Sweison, Jeff
APPLICANT: Kamb, Alexander
APPLICANT: Harshman, Keith D.
APPLICANT: Harshman, Keith D.
APPLICANT: Shattuck-Eidens, Donna M.
APPLICANT: Taviigian, Sean V.
APPLICANT: Wiseman, Roger W.
APPLICANT: Futreal, P. Andrew
TITLE OF INVENTION: 179-Linked Breast and
TITLE OF INVENTION: Susceptibility Gene
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24884-109347
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APPLICATION NUMBER: US 08/300,266
FILING DATE: 02-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,221
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,305
FILING DATE: 24-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,824
FILING DATE: 29-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/308,104
FILING DATE: 16-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/483,553
                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Ihnen, Jeffrey L. REGISTRATION NUMBER: 28,957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION
TELEPHONE: 202-962-4810
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                                    Skolnick, Mark
Goldgar, David
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                                                                           Miki, Yoshio
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION; 435
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                                                                                                                                                                                                                                                                                                                                                    Washington
Patent No. 5709999
GENERAL INFORMATION:
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US-08-483-553-20
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                                    APPLICANT:
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APPLICANT:
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                                                           APPLICANT
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US-08-483-553-20

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1201 New York Avenue, N.W., Suite 1000
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Simard, Jacques
Emi, Mitsuru
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Patent No. 5710001
GENERAL INFORMATION:
APPLICANT: Shattuck-Eidens, Donn
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Durocher, Francine
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, E
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US-08-487-002-20
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                                                                                                             PatentIn Release #1.0, Version #1.30
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55.8%; Pred. No. 3.4e-24;
tive 0; Mismatches 321;
                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 02-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,221
FILING DATE: 12-AUG-100*
                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,305
                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/348,824 FILING DATE: 29-NOV-1994 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/308,104 FILING DATE: 16-SEP-1994 PRIOR APPLICATION DATA:
                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,002
                                                                  IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Ihnen, Jeffrey L. REGISTRATION NUMBER: 28,957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 22
TELECOMMUNICATION INFORMATION
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
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                                                                                                                                                                                                                                                                    24-MAR-1995
                                               Floppy disk
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TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity 55.8
Matches 464; Conservative
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                               FILING DATE: 24-MAR-1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0
                                                                                        OPERATING SYSTEM:
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ORIGINAL SOURCE:
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                                                                                                             SOFTWARE:
                                                                    COMPUTER:
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PRIOR APPLICATION DATA:

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                                                                                              520 TGAGGTGGGAGGATCACTTGAACCCAGGAGACAGAGGTTGCAGTGAACCGAGATCACGCC
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APPLICANT: Miki, Yoshio
APPLICANT: Swenson, Jeff
APPLICANT: Swenson, Jeff
APPLICANT: Barshman, Reith D.
APPLICANT: Tavtigian, Shattuck-Eidens, Donna M.
APPLICANT: Tavtigian, Sea N.
APPLICANT: Futreal, P. Andrew
TITLE OF INVENTION: 179-Linked Breast and Ovarian Cancer
TITLE OF INVENTION: Susceptibility Gene
NUMBER OF SEQUENCES: 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA: 08/409,305
FILING DATE: 24-MAR-1995
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Goldgar, David E.
Miki, Yoshio
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ADDRESSEE: Venable,
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APPLICANT: Skolni
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US-08-483-554B-20
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0; Mismatches 321;
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                                                                                                                                                                                                                                                         24884-109347
                                                                   FILING DATE: 16-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,266
FILING DATE: 02-SEP-1994
PRIOR APPLICATION NUMBER: US 08/289,221
FILING DATE: 12-AUG-1994
                                                   US 08/308,104
US 08/348,824
                                                                                                                                                                                                                  NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFRENCE/DOCKET NUMBER: 2468
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA (genomic)
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Best Local Similarity 55.8%;
Matches 464; Conservative (
   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US OPFILING DAME:
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EDNESS: double
 APPLICATION NUMBER:
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                                                                  2437 actggcagaagctttca-----gaaaaccactggacggctgggcacagtggc
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APPLICANT: Futreal, P. Andrew
TITLE OF INVENTION: 179-Linked Breast and Ovarian Cancer
TITLE OF INVENTION: Susceptibility Gene
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .E: Venable, Baetjer, Howard & Civiletti, LLP 1201 New York Avenue, N.W., Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/488,011B FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,305
FILING DATE: 24-WAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,824
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shattuck-Eidens, Donna M.
Tavtigian, Sean V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION OF SEP-155.
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289, 221
TING DATE: 12-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/308,104
FILING DATE: 16-SEP-1994
PRIOR APPLICATION DATA:
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IBM PC compatible
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Kamb, Alexander
Harshman, Keith D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Skolnick, Mark H.
Goldgar, David E.
Miki, Yoshio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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STATE: DC
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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APPLICANT:
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APPLICANT:
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Pred. No. 3.4e-24;
0; Mismatches 321;
    24884-109347-09
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0
REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
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ilarity 55.8%;
Conservative 0
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                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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US-08-488-011B-20
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Best Local
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US-08-850-727-20

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2654
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APPLICANT: Futreal, P. Andrew
TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer
TITLE OF INVENTION: Susceptibility Gene
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
2604 gccaggcgtggtggcacaagcctagaatcccagctacttgggaggctgagg
                       939 ACTAGGCGTGGTGTACGCCTGTAGTCCCCAGCTACTCGGGAGGCTGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Venable, Baetjer, Howard & Civiletti,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/850,727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1201 New York Avenue, N.W., Suite 1000 CITY: Washington
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Kamb, Alexander
Harshman, Keith D.
Shattuck-Eidens, Donna M.
Tavtigian, Sean V.
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APPLICATION UNBER: US 08/483,554
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,824
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
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                                                                                                                                        Sequence 20, Application US/08850727
Patent No. 6162897
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
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                                                                                                                                                                                                    Skolnick, Mark H.
Goldgar, David E.
Miki, Yoshio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 12-AUG-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 6769 base pairs
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ORIGINAL SOURCE:
ORGANISM: Homo sapiens
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
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STRANDEDNESS: double
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                    RESULT 14
US-08-850-727-20
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                                                                              1869 aaaaattagctgggcgtggtggcatgcatccacaatcccagctactggggaggctgaggc 1928
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Length 6769;
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                                        Indels
  6.2%; Score 165.4; DB 4; 55.8%; Pred. No. 3.4e-24;
                                        0; Mismatches 321;
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; GENERAL INFORMATION:
; APPLICANT: Shattuck-Eidens, Donna 1
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Emi, Mitsuru
Nakamura, Yusuke
Durocher, Francine
                    Best_Local Similarity 55.89
Matches 464; Conservative
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    Query Match
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in the 17q-Linked Breast and Ovarian Cancer
Susceptibility Gene
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                                                                                                                                                                        ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP STREET: 1201 New York Avenue, N.W., Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PatentIn Release #1.0, Version #1.30
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ER: 24884-109347
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APPLICATION DATA:
APPLICATION NUMBER: US 08/348,824
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08-308,104
FILING DATE: 16-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,266
FILING DATE: 02-SEP-1994
PRIOR APPLICATION NUMBER: US 08/300,266
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Theory To Ferent NAME: Theory Treferent NAME: T
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APPLICATION NUMBER: PCT/US95/10202
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                                                                                                                                                                                                                                                                                                                                                                                                                                               IBM PC compatible
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APPLICATION NUMBER: US
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08//
FILING DATE: 24-MAR-1995
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TYPE: nucleic acid
STRANDEDNESS: double
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TITLE OF INVENTION: IN V
TITLE OF INVENTION: SUSTINEER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC OPERATING SYSTEM:
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CITY: MC.
STATE: DC
COUNTRY: USA
TD: 20005
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MOLECULE TYPE:
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PCT-US95-10202-20
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                                                                   340 AGCTGGGCGCAGTGGCTCTTGCCTGTAATCCCAGCACTTTGGGAGGCCAAGGCGGGTGGA 399
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700 AAAAAAAAGTAATGTTGGGCTTTTAAATACTCGTTCCTATACTAAATGTTCTTAGGAGTG 759
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Human Rab protein,	Human death-associ	Human colorectal c	Human colorectal c	Human TANGO 292 CD	Human glycosyl sul	Human colorectal c	Human DNA fragment	Nucleotide sequenc	Human DNA fragment	Human purH dene de
ID		AAS00624	AA157790	AA157791	AAF29453	AAD02697	AAI57673	AAZ38992	AAH74642	AAD02498	AAA28150
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Talkelmer's disease, Parkinson's disease, anyotrophic lateral sclerosis, retinitis pigmentosa, and cerebellar degeneration, myelodysplastic syndromes such as aplastic anaemia, ischaemic injuries such as myocardial infarction, stroke, and reperfusion injury, toxin-induced diseases such as alcohol-induced liver damage, cirrhosis, and lathyrism, wasting diseases such as cachexia, viral infections, and osteoporosis. They can also be used to stimulate cell proliferation for use in transplantation or to produce cells to fight an infection or a cancer or to correct a genetic defect in a disease such as sickle cell beta thalassemia, cystic fibrosis or Huntington's chorea. Antagonists can be used to prevent or treat a disorder associated with cell proliferation e.g. cancers or inflammation, e.g. Addison's disease, adult respiratory distress syndrome, allergies, asthma, atherosclerosis, bronchitis, cholecystius, diabetes mellitus, emphysema, attopic demmatitis, dermatomyositis, diabetes mellitus, emphysema, attopic demmatitis, glomerulonephritis, coult, Graves' disease, hypereosinophilia, irritable bowel syndrome, lupus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RABP-3. The Rab proteins, RABP-1, RABP-2 and RABP-3 are involved in vesicle trafficking, cell function, and cell differentiation. The RABP polypeptides, DNAs and agonists can be used to prevent or treat a disorder associated with an increase in apoptosis, e.g. infectious or genetic immunodeficiencies, neurodegenerative diseases such as
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the DAXX gene can be identified by comparing the frequency of the genotype or haplotype in a population exhibiting the trait with that of a reference population. A higher frequency in the trait population indicates an association. Methods involving genotyping or haplotyping of the DAXX gene of an individual can lead to prediction of haplotype palrs for the DAXX gene of related individuals, and may be useful in studying the expression and biological function of DAXX, as well as in developing drugs targeting this protein. Polymorphic variants of DAXX are useful in studying the effect of the variation on the biological activity of DAXX is well as on the binding affinity of candidate drugs targeting DAXX for the treatment of autoimmune diseases and other immune disorders. Polymorphism is also useful for studying population diversity, anthropological lineage, paternity testing, forensic applications, and can indentifying associations between the DAXX genetic variation and a trait such as level of drug response or susceptibility to disease. DAXX proteins may be used to measure binding affinities of one or more

proteins may be used to measure binding aff candidate drugs targeting the DAXX protein.

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New human death-associated protein 6 (DAXX) gene variants comprising 19 polymorphic sites useful in studying the effect of variation on the biological activity of DAXX and in developing drugs targeting the
 polymorphism; haplotype pair; human;
Death-associated protein 6; DAXX; polymorphism; haplotype pair; h
Immune disorder; autoimmune disease; population diversity; ds;
paternity testing; anthropological lineage; forensic application.
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The sequence represents a DNA encoding human death-associated protein 6 (DAXX). This gene may comprise one or more polymorphisms at specific nucleotide positions to form one of nineteen possible polymorphic variants. Associations between a trait and a genotype or a haplotype of

Claim 1; Fig 1; 97pp; English.

protein

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2000US-0224518.
2000US-0224519.
2000US-0225213.
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2000US-0225266.
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Disclosure; SEQ ID NO: 327; 522pp + Sequence Listing;
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number of colorectal cancer antigens. These are shown in AAA157619 and AAA3869-AAA48641. These can be used in the diagnosis, prevention and treatment of cancer of the colon and/or rectum. The present sequence is a colorectal cancer antigen genomic sequence. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                         12999 gcttttaatgggaagaagtaatgaagatatcagaaaggtatgttgaggatagactggatg 13058
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tive 0; Mismatches 948;
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Best Local Similarity 31.8
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The present invention provides the protein and coding sequences of

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                                                gggcaatgtagtgag----accccccatctctacaggaaacaataaaatacaataaaa 13893
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                                                                        aatgcagacacgaaggtgcaaagtgaagctgccagtcttgcaaaagatgtaacttgtcac 2270
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                         tagcattgaagccagcctgtagcctgaaagcctttgctttgagggcaggtctttccccaa
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The present invention provides the protein and coding sequences of a number of colorectal cancer antigens. These are shown in AAAIS7547-AAIS7619 and AAM38569-AAM38641. These can be used in the diagnosis, prevention and treatment of cancer of the colon and/or rectum. The present sequence is a colorectal cancer antigen genomic sequence. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the colon and rectum including colorectal cancers and also for testing and detection e.g. diagnosis -
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Sequence 32152 BP; 8332 A; 7335 C; 7256 G; 9229 T; 0 other

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Human; INTERCEPT 217; INTERCEPT 297; TANGO 276; TANGO 292; TANGO 325;
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                               Indels
 22;
Score 195.6; DB 22;
Pred. No. 6.9e-30;
0; Mismatches 334;
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The present sequence is given in a specification relating to isolated human proteins designated INTERCEPT 217, INTERCEPT 297, TANGO 276, TANGO 292, TANGO 331 and TANGO 332. These proteins are useful as modulating agents or as targeting agents for developing agents to regulate cellular processes e.g. growth, proliferation, survival, differentiation and activity of human tissues. Diseases which can be diagnosed, prevented and treated by administration of these polypeptides, their nucleic acids and modulators include cancers, inflammatory classis. Nucleic acids encoding the isolated proteins can be used to express the proteins in a host cell in gene therapy applications. Antisense molecules or ribozymes can be used to inhibit expression of the proteins in target cells. Fragments of the nucleic acid molecules encoding the isolated proteins are used as hybridisation probes and as
                                                                                                                                                                                                                                                                                                                                                               Isolated human proteins are used for diagnosis, treaument with prevention of cancers, inflammatory disorders, cardiac disorders e.g.
TANGO 331; TANGO 332; cytostatic; antiinflammatory; antiarrhythmic; antipsoriatic; gene therapy; cancer; inflammatory disorder; cardiac disorder; arrhythmia; skin disorder; psoriasis; ss.
                                                                                                                                                                                                                                                                                                 Barnes TS;
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                                                                                                                                                                                                                                                                                               Sharp JD,
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                                                                           Homo sapiens
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3; 1475 tttcagaagacctgaggaggctgccttgtctccattgccgccttctgtggaggatgcagg 758 Gaps agaaaagagagtgcaatgaagaactttgcaattatgaggaagccagagagtttttgtgga 519 agatggcaacagagagagaaatagatgttatgggccttctgactggattaattgctgctgg agtatttttggttatttttggattacttggctactatctttgtatcactaagtgtaatag 7.2%; Score 192.4; DB 22; Length 2498; 31.2%; Pred. No. 2.1e-29; tive 0; Mismatches 974; Indels 5; al Similarity 31.2 444; Conservative Query Match Best Local Matches 44 1296 399 1356 579 1476 639 459 δ g ò q οy g ò g δ a δ

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                                                                                                     polyarteritis nodosa; polymyositis; systemic sclerosis; dermatitis; glomerulonephritis; myasthenia gravis; Sjogren's syndrome; adrenalitis; Hashimoto's disease; Grave's disease; hypoparathyroidism; anaemia; demyelinating disease; cirrhosis; ulcerative colitis; allergic rhinitis; myocarditis; adult respiratory distress syndrome; eczema; psoriasis; asthma; hypersensitivity; rheumatic fever; tissue rejection;
                                                                              Human, glycosyl sulfotransferase-4; GST-4; immunosuppressive; therapy; selectin binding inhibitor; gene therapy; inflammation; systemic lupus erythematosus; SLE; rheumatoid arthritis; diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                'note= "Portion of 5' untranslated region (5'UTR)"
                                                                                                                                                                                                                                                                                                                                                                                                                   the ORF
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(GST-4alpha)"
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83348..96412
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            AAD02697
       RESULT
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CGT is a type 2 membrane protein useful for inhibiting a binding event between a selectin and a selectin ligand, which comprises contacting the selectin with a non-sulphated selectin ligand, GST and a small molecular agent that inhibits the sulphation activity of GST. GST is also useful in inhibiting a selectin mediated binding event. GST is useful in gene therapy to treat disorders such as acute or chronic inflammation. Systemic lupus erythematosus (SID), rheumatoid arthritis, polyarteritis nodosa, polymyositis, dermatomyositis, systemic sclerosis, diabetes, glomerulonephiritis, myasthenia gravis, Syogren's syndrome, Hashimoto's anaemia, demyelinating disease, adrenalitis, hypoparathyroldism, pernicious anaemia, demyelinating diseases, cirrhosis, ulcerative colitis, dermatitis, myocarditis, regional enteritis, adult respiratory distress conforme, infantile eczema, psoriasis lichen planus, allergic rhinitis, bronchial asthma, hypersensitivity, rheumatic fever and tissue rejection curring transplantation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 54991 aaaaattagctgggcgtggtggcagacgcctgtaatcccagctacttgggaggctgaggc 55050
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                                                                                                                                                                                                                                                                                                                                                                            /note= "Portion of 5' untranslated region (5'UTR)"
98474..99661
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/note= "Includes 17 base pairs of 5'UTR, the ORF
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/product= "Human glycosyl transferase-4beta
(GST-4beta)"
99662..99968
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98457..99968
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57.3%; Pred. No. 1.2e-28;
tive 0; Mismatches 287;
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96485..98456
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98457..98473
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13-JUL-2000; 2000US-0593828
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Best Local Similarity 57.3
Matches 451; Conservative
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17-MAR-2000;
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                     55436 caagctagcagaaaccatttgccataaaaataagagcaaaaccaagaggaagcggaaagt 55495
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       caaagtga-agctgccagtcttgcaaaagatgtaacttgtcacgaaggccacgagtggca 2287
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                                                                                           2169 gtagcctgaaagcctttgctttgagggcaggtctttccccaaaatgcagacacgaaggtg
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                                                   2049 ttaggtgcagggtgtcctctgttattcactgagaccgtgccccggttatgaggttgtacc
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2000US-0180628.
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04-FEB-2000;
24-FEB-2000;
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2000US-0215135.
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The present invention provides the process and of colorectal cancer antigens. These are shown in number of colorectal cancer antigens. These can be used in the AAI57647-AAI57619 and AAM3869-AAM38641. These can be used in the diagnosis, prevention and treatment of cancer of the colon and/or rectum diagnosis, prevention and treatment cancer antigen genomic sequence.
                                                              The present sequence is a colorectal cancer antigen genomic sequence. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                             Sequence 32199 BP; 9884 A; 7746 C; 6845 G; 7724 T; 0 other;
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Best Local Similarity 55.19
Matches 433; Conservative
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           13-OCT-2000; 2000US-023937.
20-OCT-2000; 2000US-023937.
20-OCT-2000; 2000US-024936.
20-OCT-2000; 2000US-0241785.
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20-OCT-2000; 2000US-0249211.
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08.DEC-2000;
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                                                                                                                                                28138 aaaaattagccaggcgtggtggtggagcctgtaatcccagctactcaggagactgaggc 28197
                                                                                                                                                                                                                                                                                                                                                     28616 accatctgacaaactctgaaaggactcctccagcacaagcccaactccacctcaagactc 28675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28676 ggtcacaga--ggcctttggaagacaagcctttgagccccacccacccatccctgaagc 28733
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                                                                                                                                                                                                                                                                                                                                                                                                      2108
                                                                                               1869 aaaaattagctgggcgtggtggcatgcatccacaatcccagctactggggaggctgaggc 1928
                                                   4; Gaps
                                                                                                                                                                                                  2049 ttaggtgcagggtgtcctctgttattcactgagaccgtgccccggttatgaggttgtacc
                                                                                                                                                                                                                                                                                                                                                                                                                                                       28318 acaagaaccatataatagaagcgcctcccaccaccactgtgtcctcccattcctccctgcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28378 ccgtcccacct-tccccagagacctcccctctgaatggccctcaccttgtgagtcatcag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cacttgaggtcaggagttccagaccagcctggccaacatggtgaaaccccatctctacag
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22; Length 32199
                                                 Indels
                                              0; Mismatches 349;
Score 189.6; DB :
Pred. No. 1.1e-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence encodes a human DNA fragmentation factor, designated DFF40. Also described are: (1) a method of inducing apoptosis in a cell comprising providing the cell with DFF40 which results in apoptosis; (2) a method for inhibiting the growth of a cancer cell comprising contacting a cancer cell with a DNA fragmentation factor designated DFF40 under conditions permitting the uptake of the DNA cragmentation factor by the cell where the presence of the DFF40 into the cell induces apoptosis; (3) a method for treating cancer comprising: (a) encoding a DFF40 DNA fragmentation factor; and (b) a promoter active in the tumour cell, where the promoter is operably linked to the region encoding the DNA fragmentation factor, under conditions permitting the uptake of the nucleic acid by the tumour cell; (4) a method of contact and uncitional DNA fragmentation factor. An expression construct encoding a DNA fragmentation factor. An expression construct encoding a DNA fragmentation factor. DFF40 is used to inhibit the contact of th
                                                                                                                                                             factor; DFF40; DFF45; apoptosis; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1869 aaaaattagctgggcgtggtggcatgcatccacaatcccagctactggggaggctgaggc 1928
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA fragmentation factor DFF40 involved in apoptosis and related nolvential entitle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.1%; Score 189.4; DB 21; Length 2839; 57.1%; Pred. No. 8.3e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41;
                                                                                                                        Human DNA fragmentation factor DFF40 nucleotide sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP; 642 A; 699 C; 750 G; 737 T; 11 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             growth of a cancer cell, especially in humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     296;
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                    BP
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                AAZ38992 standard; cDNA; 2839
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                                                                                      (first entry)
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                                                                                                                                                             fragmentation
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Best Local Similarity
Matches 448; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                             Liu X;
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                                                                                                                                                             DNA
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1989
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                                                                                                                                                                                                                                                                                                                                                                                                                             TTATCCCTACTGACCCGTATGACCAGGTACTCACAGACATCCAACGAGTACCCCAGAGCT 1635
                                                                                                      CTTTTGGGCATTTAGAAGATCAAGAGGATGGAGCTGCCCATTTGCCATGGAAAGGGAGAC
                                                                                                                                                 gtagcctgaaagcctttgctttgagggcaggtctttccccaaaatgcagacacgaaggtg
                                                                                                                                                                                                                                  caaagtgaagctgccagtcttgcaaaagatgtaacttgtcacgaaggccacgagtggcag
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                                                                                                                                                                                                                                                                                                                gagataagagacaatcataaggggagatatcagagaaaatcgtaaggggagcagatggtt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA fragmentation factor; DFF40; DFF45; apoptosis; DNase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product= "DNA fragmentation factor 40 (DFF40)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleotide sequence of human DNA fragmentation factor 40
                                                                                                                                                                                    1848 CCAG-CAGAGAGCTGATACATAAACAACTTGTCCCTC----
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132..1148
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AAH74642/c
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Query Match
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                                                                              DNA fragmentation factor polypeptides and polynucleotides, useful inhibiting the growth of cancer cells, as well as for inducing
                                                                                                                                                                         The present sequence encodes a human DNA fragmentation factor subunit of 40 kDa, designated DFF40. The specification also describes DFF45. DFF40 is capable of inducing apoptosis, and may contain a nuclear localisation fragment. DFF45 acts as a molecular chaperone to direct the folding of DFF40. Although all DMSes activity; as associated with DFF40, DFF activity only occurs once DFF40 is complexed with DFF45. The DFF polypeptides and polynucleotides are useful for inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                       the growth of cancer cells, and for inducing apoptosis of cells.
                                                                                                                                                                                                                                                                                                                                                                       Length 2839;
                                                                                                                                                                                                                                                                                                                                                                                                       41;
                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches 296; Indels
                                                                                                                                                                                                                                                                                                                     Sequence 2839 BP; 644 A; 701 C; 755 G; 739 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1848 CCAG-CAGAGAGCTGATACATAAACAACTTGTCCCTC------
                                                                                                                                                                                                                                                                                                                                                                     Score 189.4; DB 22;
Pred. No. 8.3e-29;
                                                                                                                                          Claim 18; Page 44-45; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                     7.18;
57.18;
                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 57.1
Matches 448; Conservative
                             WPI; 2001-496169/54
                                                                                                          apoptosis of cells
                                                P-PSDB; AAG63592
Liu X;
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 Nang X,
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comprising 40kDa and 45kDa subunits. DFF45 acts as molecular chaperone to facilitate the appropriate folding of DFF40 and acts as a molecular chaperone to facilitate the appropriate folding of DFF40 and acts as an inhibitor for DFF40 and DFF45 are used in gene therapy. The modulators of human DFF40 activity are useful for inducing apoptosis and for treating hyperproliferative disorders such as restenosis, psoriasis, metastatic tumours, angiogenesis and benign and malignant neoplasias. They are also used for treating cancers of the brain (glioblastoma, astrocytoma, oligodendroglioma and ependymoma), lung, liver, spleen, kidney, lymph node, pancreas, small intestine, blood cells, colon, stomach, breast, endometrium, prostate, testicle, ovary, skin, head and neck, oesophagus, bone marrow, blood, other tissue and multi-drug resistant cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA fragmentation factor; DFF; apoptosis; molecular chaperone; nerapy; hyperproliferative disorder; therapy; tumour; restenosis; is; angiogenesis; cancer; cytostatic; neoplasia; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying modulator of human DNA fragmentation factor 40, for treating cancer, involves contacting cell or cell-free composition comprising DFF40 with candidate substance and comparing apoptosis with
1529 CACCTGAGGTCAGGAGTTTGAGACCAGCCTGACCAACATGGTGAAACCCCGTCTCTACTA 1470
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                                                                                                                                     2589 aaaatataaaaattagccaggcgtggtggcacaagcctagaatcccagctacttgggagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= a
/product= "DNA fragmentation factor 40 (DFF40)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human DNA fragmentation factor 40 (DFF40) cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Column 77-80; 52pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene therapy; hyperproliferative psoriasis; angiogenesis; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAD02498 standard; cDNA; 2839
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DB 22; Length 2839;

Score 189.4;

7.18;

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Location/Qualifiers
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23277..23384
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24841..24926
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24927..25956
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2560..8091
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                                                                                                                                               1968 TGAATGTCCTTGTATGTTCTTTACGGAGTATAAACATCGTACCCCCAAAGCATGACACCT 1909
                                                                                                                                                                                                  2169 gtagcctgaaagcctttgctttgagggcaggtctttccccaaaatgcagacacgaaggtg 2228
                                                                                                                                                                                                                                    caaagtgaagctgccagtcttgcaaaagatgtaacttgtcacgaaggccacgagtggcag 2288
                                                                                                                                                                                                                                                                                     1754 AGCAAACCCAACGCTGGTGAAACCAGAGAACAGAATTCCTCAGGCCCAGAGAATTC 1695
          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; purH; biallelic marker; single nucleotide polymorphism; SNP; diagnosis; prevention; treatment; prostate cancer; tumour; chromosome 1q34-q35; ds.
                                                                                                                                                                                                                                                  --AAGCAAGGTGGCCAACTTCAGCCATGACACCATTTGAGTATGGTGACCACATTACATG
                                                                                                                                                                                                                                                                    ggagagctgtcccacatttgcggaagtggctatgtgaggacggggaggcgggtccctta
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                                                                                                                                                                                                                                                                                                                       1694 TTATCCCTACTGACCCGTATGACCAGGTACTCCAGACATCCAACGAGTACCCAGAGCT
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          41;
57.1%; Pred. No. 8.3e-29;
ive 0; Mismatches 296; Indels
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        448; Conservative
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ctgag 2653
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ID AAA281.
AC AAA281.
XX AAA281
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/*tag= bd primer_bind complement (1642916266) /*tag= be primer_bind 1659916617	primer_bind complement (1703017049) /*tag= bg primer_bind 1813118150		/*tag= bj 2310023118 /*tag= bk	<pre>primer_bind complement (2313023149) primer_bind complement (2351223530)</pre>	/*tag= bm 2582225840 /*tag= bn	<pre>primer_bind complement (2622226241) /*tag= bo primer_bind 3033230352</pre>		<pre>primer_bind 3091830935 primer_bind complement (3139031408)</pre>	/*tag= bs primer_bind 34780.34799 /*tag= bs		3659336610 /*tag= bv	primer_bind comprement (5/01/5/030) /*tage=ment (5/01/5/030) primer bind 3706037080		tch 7.0%;	<pre>similarity 56.8%; Pred. No. 5.7e-28; 2; Conservative 0; Mismatches 320;</pre>	aaaaattagctgggcgtgggtgcatccacaatcccagctactggggaggctgaggc	AAAAATTAGCCGAGCGTGATGGCGGGCACCTGTAATCCCAGCTACTGGGGAGGCTGAGGC	1929 atgagaateggttgaaccggggaggcagaggttgaagtgagcggagcg	1989 etccagectggactacagagegagetetateteaaaaaaaaaa		2040 aaaagtaacttaggtgcaggggtgtcctctgttattcactgagaccgtgcccggttatga 209	7412 GATGCCATATCAAGTGAGTGAAGACATAAAAGACTGTTTAATAAAGTGGTGTTGCTATTG 735	2100 ggttgtaccagaaagcaagtattcactatgcacactattcaccgctcaccctagcattga 2159	7352 GAATAACGGGTTAAACCCAAACAAAATATTCCTTATGAATCAAAGGTTTAGCATTTA 7293	2160 agocagoctgtagoctgaaagoctttgotttgagagagaggtettteoceaaaatgeagae 2219 720 aaaaancanocaancanocaa a namaaanaancaancanocaannonnaaanaa 724 720 aaaaancanocaanocaanocaaanaanaa 724	220 acgaaagtgcaaagtgaagctgccagtcttgcaaaagatgtaacttgtcacgaaggccac
FTF	FT	FT FT	FT FT	FT FT	FT FT	EEEE	FT	FT FT	FT FT	FT	FI	TE	FT FT	ono.	Bes	Qy	qa ,	රු අ	Qy	qq	Qy	Dp	Οy	Dp	Qy dg	oy ,
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												variation	variation	variation	variation	variation	variation						primer_bind	primer_bind	primer_bind	primer_bind

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Disclosure; Page 973-975; 1592pp; English

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human; airway disorder; bronchoconstriction; lung inflammation; surfactant depletion; respiratory; bronchodilator; antinflammatory; immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic; respiratory obstruction, pulmonary obstruction; impeded respiration; surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS; respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis; pulmonary hypertension; emphysema; pulmonary transplantation rejection; chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers and respiratory obstructions -
                                                                                                                                                                                                                                                                  2519
                                                                                                                                                                                                                                                                                                                                                                                                                                                        6827
7233 AAGATTGAGAGTTCTGATTACAGAAATGTTAAAAAAAGTTTTACATGGGAAAAAAG 7174
                                                                                                                                                                                                                             -----GACTTTATAAGTTGTAATGGTGTGTAAAAATGCCCACAATATATAAGAAAAAT 7006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human low adenosine antisense oligonucleotide related sequence #2689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           adenosine antisense oligonucleotide; phosphorothioate; allergy;
                                                                                                                                                                                                                                                                                                                                                                                                                 2579 atototacagaaaatataaaaattagocaggogtggtggcacaagootagaatoocagot
                                                                                                                                                                                                                                                                                                                                                                CGAATGGATCACCTGAGGTAAGGGAGTTCCAGACCAGCCTGACCACATGGTGAAACCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                      6885 GCCTCTACTAAAAATA-CAAAATTAGCCAGGCATGGTGGGGGCATGCCTATAATCCCAGCT
                                          gagtggcagggagagctgtcccacatttgcggaagtggctatgtgaggacgggggaggcg
                                                                           7173 TAAACTAGAAAAATAATCACACAATGTGACAAAGGGTCAAGTGAAGGACAGTAATT
                                                                                                                ggtcccttagagataagagacaatcataaggggagatatcagagaaaatcgtaaggggag
                                                                                                                                                  7113 AATCCATATCACAAAGCAGACCCCTAGAAAGTCATAACCACGAACACTCTGGCA----
                                                                                                                                                                                          cagatggttgtcaagagaataggctgaccatcgaaggactggcagaagctttcagaaaac
                                                                                                                                                                                                                                                                 2460 cactggacggctgggcacagtggcttaggcctgtaatcccagcactttgggaggctgacg
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(NYCE/) NYCE J W.
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The present invention describes low adenosine (A) content antisense oligonuclectides and compositions (I) comprising them. In the antisense coligonuclectides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, antifilammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonuclectides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and nor specific enzymes, binding proteins, adenosine melecules and their receptors, cytokine and chemokine receptors, adenosine receptors, bradykinin receptors, central
                                                                                                                                                                                                                                                                                                                                                                        receptors, CNS and peripheral instructs and increase system peptide transmitters, defensins, growth factors, vasoactive peptides and transmitters, defensins, growth factors, vasoactive peptides and antisense oligonucleotides may be used in this way to treat disorders. Including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(les) and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AART8434 to AART8433 represent human polynucleotide transments and antisense oligonucleotides used in the exemplification of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antisense oligonucleotide (ON) with low adenosine (up to 15%), which targets nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antinflammatory, antiallergic, antiasthmatic, cytostatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation.
                                                                                                                                                         5203
                                                                                                                                                                                                                                                                                                                                                                                                                Human; adenosine receptor; low adenosine antisense oligonucleotide; phosphorothioate; impaired respiration; inflammation; allergy; allergic disease; bronchoconstriction; inhibitor; antiinflammatory; antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway; lung disease; ischaemic condition; pulmonary vasoconstriction; asthma; respiratory distress syndrome; pain; cystic fibrosis; emphysema; pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
                                                                                                                                                                                                       5143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        impaired airways, including lung disease and diseases whose secondary
                                                                                                                                                                               2580 tctctacagaaaatataaaaattagccaggcgtggtggcacaagcctagaatcccagcta
                                                                                                                                                                                            5202 TCTCCACAAAAATACAAAAAATTAGCCAGGCATGCTGGCACACACTGTGTTCTCAGCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstriction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia or
2400 cagatggttgtcaagagaataggctgaccatcgaaggactggcagaagctttcagaaaac
                                                                                2460 cactggacggctgggcacagtggcttaggcctgtaatcccagcactttgggaggctgacg
                                                                                                caggtgaatcacttgaggtcaggagttccagaccagcctggccaacatggtgaaacccca
                                                          The present invention describes a new composition comprising an
                                                                                                                                                                                                                                                                                                                                                                                           Human adenosine receptor related polynucleotide SEQ ID NO: 2689.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
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erice allittic the lings of a subject they can be used for treating e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukaemias, lymphomas, carcinomas, and cancers which may metastasise to the lungs, including breast and prostate cancer. The reduction of the adenosine content of the ONs reduces side effects. The A-containing ONs break down with the release of deoxyadenosine which activates adenosine receptors causing bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the incledition sequences given in the sequence listing from the present invention, which correspond to SEQ ID NO:1 to 185, but the sequences are also called SEQ ID NO:1 to 185, but the sequences are also called SEQ ID NO:1 to 185, but the sequences called sequences. SEQ ID NO:1 to 185 sequences are also ealted SEQ ID NO:1 to 185. but the present invention, W.B. Sequences given in the disclosure of the present invention do not match up with their corresponding SEQ ID NO: sequences
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effects afflict the lungs of a subject. They can be used for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1869 aaaaattagctgggcgtggtggcatgcatccacaatcccagctactggggaggctgaggc
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4.8e-28;
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Pred. No. 4.8e-
0; Mismatches
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2580 tctctacagaaaatataaaaattagccaggcgtggtggcacaagcctagaatcccagcta
                                                                                 5142 crcaggaggccaagg 5128
                                                       2640 cttgggaggctgagg 2654
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AAF21124 standard; DNA; 10032 BP. AAF21124/

(first entry) 14-MAR-2001 AAF21124;

Human low adenosine antisense oligonucleotide related seguence #2691

Low adenosine antisense oligonucleotide; phosphorothioate; allergy; human; alivayd idsorder; bronchoconstriction; lung inflammation; surfactant depletion; respiratory; bronchodilator; antiinflammatory; immunosuppressive; antiasthmatic; analgesic; hypotensive, cytostatic; respiratory obstruction; pulmonary obstruction; impeded respiration; surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS; respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis; pulmonary hypertension; emphysema; pulmonary transplantation rejection; chronic obstructive pulmonary disease; pulmonary infection; bronchitis; cancer; ss.

Homo sapiens

WO200062736-A2

26-0CT-2000

2000WO-US08020 24-MAR-2000; 99US-0127958 06-APR-1999;

EAST CAROLINA. (UYEC-) UNIV (NYCE/) NYCE

Nyce JW;

WPI; 2000-679539/66.

Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers and respiratory obstructions -

Disclosure; Page 975-978; 1592pp; English.

The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, antinfilammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with lung/respiratory disorders and mallighancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adenosine receptors, cytokine and chemokine receptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, defensins, growth factors, vasocative peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction

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and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAF18434 to AAF21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of
                                                                                                                                                                                                                                                                                                           aaaaattagctgggcgtggtggcatgcatccacaatcccagctactggggaggctgaggc 1928
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                                                                                                                                                                                                                                           Length 10032;
                                                                                                                                                                                      Sequence 10032 BP; 2342 A; 2486 C; 2643 G; 2561 T; 0 other;
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                                                                                                                                                                                                                                          DB 21;
                                                                                                                                                                                                                                        Score 185.8; DB 21;
Pred. No. 5.1e-28;
0; Mismatches 337;
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Human; adenosine receptor; low adenosine antisense oligonucleotide; phosphorothioate; impaired respiration; inflammation; allergy; allergic disease; bronchoconstriction; inhibitor; antiinflammatory; antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway; lung disease; ischaemat condition; pulmonary vasoconstriction; asthma; respiratory distress syndrome; pain; cystic fibrosis; emphysema; pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstriction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia or
                                                                                                                                                                                                                                  Human adenosine receptor related polynucleotide SEQ ID NO: 2691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
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                                     AAA35002 standard; DNA; 10032 BP
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continued of the composition of the control obstructive carcinomas, and concers which may metastasise to the lungs, including concerns the concern of the con present invention describes a new composition comprising an

Search completed: January 11, 2002, 17:19:41 Job time: 29533 sec

Sequence 10032 BP; 2342 A; 2486 C; 2643 G; 2561 T; 0 other;

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                                         1869 aaaaattagctgggcgtggtggcatgcatccacaatcccagctactggggaggctgaggc 1928
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    DB 21; Length 10032;
                        Indels
             Pred. No. 5.1e-28;
0; Mismatches 337;
Score 185.8, DB 2
     7.08;
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A1239858 qh33301.x
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Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                              AI633353 ts96b09.x
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AQ223799 538 bp DNA GSS 20-SEP-1998 HS_2218_A1_C06_MR CIT Approved Human Genomic Sperm Library D F sapiens, genomic clone Plate=2218 Col=11 Row=E, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence-tagged connectors: A sequence approach to mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
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High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
TEL: (206) 616-3887
Email: jwallaceu.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
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Location/Qualifiers
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/organism="Homo saplens"
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AI766998 wh97C08.x
AI540062 tod8968.x
AW515919 xy02C11.x
AW015376 UI-H-BIO-
AW072388 xa07d05.x
AI233613 qh37d07.x
AI682248 wa71904.x
AI47089 tm31a08.x
AW97759 EST389708
AW97753 UI-H-BII-
                                                                                                              January 11, 2002, 11:36:18 ; Search time 8779.43 Seconds (without alignments) 3248.422 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                           11351937 seqs, 5372889281 residues
                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                          US-09-820-005-3_COPY_16200_18853
2654
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Maximum Match 100%
Listing first 45 summaries
                                                                                   - nucleic search, using sw model
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AN515919
AW015316
AW012384
A1239613
AN572661
AW572661
AW977599
AW97759
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AI760998 476 bp mRNA EST 20-DEC-1999 wh97c08.xl NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2388686 3' similar to 9b:M55067 NEUTROPHIL CYTOSOL FACTOR 1 (HUMAN);, mRNA
                     /clone_lib="CIT Approved Human Genomic Sperm Library D"
                                                            /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"
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                                                                                                                                                                                      Length 538;
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                                                                                                                                                                                                                                 Indels
                                                                                                      12
                                                                                                                                                                                        DB 13;
                                                                                                                                                                                    Score 420.4; DB 13;
Pred. No. 4.3e-46;
0; Mismatches 20;
/clone="Plate=2218 Col=11 Row=E"
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                                                                                                                                                                                    15.8%;
llarity 94.8%;
Conservative (
                                      /sex="male"
                                                                                                      144 c
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Unpublished (1997)
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T 3']; double-stranded CDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    412 CAGCGTCCGTTTTCTGCAGCAGCGACCCGCCAGGCGGCGGGGCGGGACCGCAAAACCCCGGG 353
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                                                                                                                                                     /clone_lib="NCI_CGAP_CLL1"
/tissue_type="B-cell, chrohic lymphotic leukemia"
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1183 ggaatgcagggagggccgggctccgcccagggttattttctaagt 1228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52 GGAATGCAGGGAGGCCGGGCTCCGCCCCAGGGTTATTTTTAAATT 7
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1388 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 388.
                                                                                                   /organism="Homo sapiens"
                                                                                                                     /db_xref="taxon:9606"
/clone="IMAGE:2388686"
                                                                     Location/Qualifiers
                                                                                                                                                                                         /lab_host="DH10B"
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AUTHORS

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xy02c11.x1 NCI_CGAP_LVM12 Homo sapiens cDNA clone IMAGE:2851988 similar to gb:M55067 NEUTROPHIL CYTOSOL FACTOR 1 (HUMAN);, mRNA
                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host-"DH10B"
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0
                                                                AW515919.1 GI:7154001
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Best Local Similarity 93.5%;
Matches 347; Conservative C
                                                                                                                                                                                                          Tumor Gene Index
Unpublished (1997)
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                                                                                                human.
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                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
M.D., Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M. Bento Scares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.libl.gov/bbrp/image/image.html
Insert Length: 1586 Std Error: 0.00
Seg primer: -40UP from Gibco
High quality sequence stop: 378.
                                                                                                                                                                                                                                                                                                                                                                                      I 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTTM3 vector. Library is normalized, and was constructed by Bento
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 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                   /clone="IMAGE:2075102"
/clone_lib="NCI_CGAP_CLL1"
/tissue_type="B-cell, chronic lymphotic leukemia"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 478;
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Pred. No. 1.3e-34;
0; Mismatches 24;
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                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
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93.5%;
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Unpublished (1997)
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Life Technologies catalog #: 11547-015 .

Life Technologies catalog #: 11547-015 .

Life Technologies catalog #: 11547-015 .

Lone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image. Llnl.gov/image/html/iresources.shtml

Seq primer: -40UP from Glaco

High quality sequence stop: 425.
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'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="IMAGE:2851988"
/clone_lib="NCI_CGAP_Lym12"
/tissue_type="lymphoma, follicular mixed small and large cell"
                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 594)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Pred. No. 1.2e-34;
); Mismatches 24; Indels 0;
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human.
               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-remail.nih.gov
The sequence contained an oligo-dT track that was present in the oligouclectide that was used to prime the synthesis of first strand cDNA and therefore this may repersent a bonafide poly A tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the IM.A.G.E. Consortium/LLNL at:
Www-blo.llnl.gov/bbrp/lmage.html
Seq primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , Lennon & Soares (1996): Normalization and Subtraction:
Two Approaches To Facilitate Gene Discovery. Genome
Research 6, 791-806.
TAG_LIB=NIL CGAP_BR2
TAG_LISSUE=Dreast
                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 444)

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Oppublished (1997)
       AW015376 444 bp mRNA EST 10-SEP-1999
UI-H-BIO-aat-c-12-0-UI.s1 NCI_CGAP_Subl Homo sapiens cDNA clone
IMAGE:2710295 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           xa07d05.xl Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:2567625 3' similar to 9b:M55067 NEUTROPHIL CYTOSOL FACTOR 1
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 750)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                          1151 aaatgttgcttggagtggaccgaggctctgcaggaatgcaggaggccgggctccgccc 1210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE consortium (info@image.llnl.gov) for further information.
Insert Length: 1386 Std Error: 0.00
Seq primer: -40UP from Gibco
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0
Score 331.2; DB 10; Length 444;
Pred. No. 2e-34;
); Mismatches 28; Indels 0;
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/db_xref="taxon:9606"
/clone="IMAGE:2567625"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 464. Location/Qualifiers 1...750
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  12.5%;
92.6%;
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AW072388.1 GI:6027386
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                      Similarity
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tracer in a subtractive hybridization reaction. The driver was PCR-amplified coRNsA from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 72408-728711, and 729096-731399. Subtraction by Bento Sares and M. Fatima Bonaldo. 1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AI239613 441 bp mRNA EST 13-APR-1999
qh37d07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:1846861 3' similar to qb:M55067 NEUTROPHIL CYTOSOL FACTOR 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1489 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 324.
Location/Qualifiers
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Pred. No. 1.7e-34;
0; Mismatches 28; Indels
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Best Local Similarity 92.6%;
Matches 348; Conservative
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/note="Organisms pooled; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not 1; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCBI) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified CDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Scares and M. Fatima Bonaldo. " a 145 c 152 g 79 t
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IMAGE:2301654 3' similar to gb:M55067 NEUTROPHIL CYTOSOL FACTOR 1
AI682248
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
1 (bases 1 to 561)
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/clone_lib="Soares_NFL_T_GBC_S1"
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Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukarmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
1 (bases 1 to 451)
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/lab_host="DH10B"
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                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2301654"
Insert Length: 1521 Std Error:
Seq primer: -400P from Gibco
High quality sequence stop: 410.
Location/Qualifiers
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Email: cgapbs-remail.nih.gov
Life Technologies catalog #: 11547-015
DNA Sequencing by: Washington University Genome Sequencing Center
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llni.gov/image/html/iresources.shtml
Seq primer: -40UP from Gibco
High quality sequence stopp: 299.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Organ: Tymph node; Vector: pCMV-SPORT6; Site_1:
Sal1; Site_2: NotI; Cloned unidirectionally. Primer:
Oligo dT. Average insert size 1.25 kb. Life Technologies
catalog #: 11547-015#
143 c 158 g 82 t
                                                                                                                                                                                                                                                                                                                                                          /clone_lib="NCI_CGAP_Lym12"
/tissue_type="lymphoma, follicular mixed small and large
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         851 gcggggcggggcgtctgactcggccccgctctctgcccgcagaggagggggggagcgaagc 910
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                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                     Contact: Robert Strausberg, Ph.D.
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                                                               Unpublished (1997)
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                                           Tumor Gene Index
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Homo sapiens

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (bases 1 to 337)

Hegde, P., Oi.R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt, J.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and Quackenbush, J.

Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray

Unpublished (2000)

A. Contact. John Quackenbush

The Institute for Genomic Research

The Institute for Genomic Research

Thel: 301 838 9528

Fax: 301 838 0208

Email: johnq@tigr.org
                                                                     AW977599 337 bp mRNA EST 02-JUN-2000
EST389708 MAGE resequences, MAGO Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
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/clone_lib="mAGE resequences, MAGO"
/note="Vector: pBluescriptSKm"
111 c 108 g 58 t
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illarity 97.6%;
Conservative
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Best Local Similarity
Matches 323; Conserv
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                                                                                                                                                                                        M.D., Louds M. Staudt, M.D., Ph.D., COLN Library Preparation: M. Bento Scares, Ph.D. CDNA Library Preparation: M. Bento Scares, Ph.D. CDNA Library Preparation: M. Bento Scares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/Amage/image.html
Insert Length: 705 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 460.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo." I others
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             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 625)
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Tumor Gene Index
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Lissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        971 gctgcagcgagagcaccaagcggaagctggcgtctgccgtctgaggctggagcgcagtcc 1030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1031 ccagctagcgtctcggcccttgccgcccgtgcctgtatatacgtgttctatagagcctg 1090
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/tissue_type="B-cell, chronic lymphotic leukemia"
/lab_host="DH10B"
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/clone="IMAGE:2158166"
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AW207763 311 bp mRNA EST 02-DEC-1999
UT-H-BI1-aff-b-10-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone
IMAGE:2721379 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                             952 gccgacctcatcctgaaccgctgcagcgagagcaccaagcggaagctggcgtctgccgtc 1011
                                                                                                                                                                                                                    1012 tgaggetggagegeagteeceagetagegteteggeeettgeegeeeegtgeetgtatat 1071
                                                                                                                                                                                                                                                                                          1072 acgtgttctatagagcctggcgtctggacgccgagggcagccccgaccctgtccagcgc 1131
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 Length 337;
                                       Indels
Score 318.2; DB 10;
Pred. No. 1.1e-32;
0; Mismatches 8;
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AW207763.1 GI:6507259

VERSION

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human.
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A1436579/C
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//dap.nost="Whitub (Line Technologies)
//dap.nost="Whitub (Line Technologies)"
//dap.nost="Whitub (Line Technologies)
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The sequence contained an oligo-dr track that was present in the oligonuclectide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution: N.B. Caches Lab Clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                www-bio.lnl.gov/bbrp/image/image.html
Seq primer: M13 Forward
POLYA=Yes.
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                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                        Unpublished (1997)
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T.3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into Lie Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."

169 c 194 g 111 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nlh.gov
Tissue Procurement: Ash Alizadeh, John Byrd, M.D.; Mike Grever,
Touis M. Staudt, M.D.; Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCL-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                goggaagctggcgtctgccgtctgaggctggagcgcagtccccagctagcgtctcggccc 1049
                         311 GGGGTGCCCCGGGGCGGACACCACCACCATGAACCGCTGCAGAGCAGAGCACACAA 252
                                                                                                                                         930 ggcggtgcccccgcggccgagcgccgacctcatcctgaaccgctgcagcgagagagcaccaa 989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="IMAGE:2129379"
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/tissue_type="B-cell, chronic lymphotic leukemia"
/lab_host="DH10B"
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Insert Length: 1255 Std Error: 0.00
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/db_xref="taxon:9606"
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High quality sequence stop: 475.
Location/Qualifiers
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Unpublished (1997)
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Location/Qualifiers
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98.3%;
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Best Local Similarity 98.3
Matches 293; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequencing Center
information can be
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I toases 1 to 877, NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA767386 877 bp mRNA EST 08-FEB-1998 nz81h11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1301925 3' similar to gb:M55067 NEUTROPHIL CYTOSOL FACTOR 1 (HUMAN);, mRNA
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Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          germinal center B cells by flow sorting (CD20+, IgD-),
                                                                                                                                                                 911 agogetetaaaaccgcagccggcggtgcccccggcggccgagcgccgacctcatcctgaacc 970
                                                                                                                                                                                        276 AGCGCTTTAAACNGCAGCCGGCGGTGCCCCCGCGGCCCGAGCGCCCGACCTCATCCTGAACC 217
                                                                                                                                                                                                                                                                  116 GCTGCAGCGAGAGCACCAAGCGGAAGCTGGCGTCTGCCGTCTGAGGCTGGAGCCCCAGCC 157
                                                                                  851 gcggggcggggggcgtctgactcggccccgctctctgcccgcagaggaggagggggagcggc 910
                                                                                                                        336 GCCAGGCGCGGCCGGGACCGCAGAGCCCCGGGAGCCCGCTCGAGGAGGAGGCGGCAGACGC 277
                                            Gaps
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Length 547;
                                          27; Indels
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10.6%; Score 281.4; DB 10; 91.7%; Pred. No. 5.7e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 445.
Location/Qualifiers
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/clone_lib="NCI_CGAP_GCB1"
                                          0; Mismatches
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Unpublished (1997)
                                          Matches 297; Conservative
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                       Best Local Similarity
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    Query Match
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CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-GGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 123 Std Error: 0.00
Seq primer: -40ml3 fwd. Error: 0.00
High quality sequence stop: 403.
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oy60a07.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:1670196 3's similar to 9b:M55067 NEUTROPHIL CYTOSOL FACTOR 1 (HUMAN);, mRNA
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provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 435)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
Unpublished (1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              952 gecgaectcateetgaaeegetgeagegagagageaeeaageggaagetggegtetgeegte 1011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1012 tgaggctggagcgcagtccccagctagcgtctcggcccttgccgccccgtgcctgtatat 1071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              237 GCCGACCTCATCCTGAACCGCTGCAGCGAGAGCACACAAGCGGAAGCTGCCTCTCT 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       177 TGAGGCTGGAGCGCAGTCCCCAGCTAGCGTCTNCGCCCTTGCCGCCCGGTGCCTGTACAT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1132 ggctcccgccaccctcaataaatgttgcttggagtggaccgaggctctgcaggaatgc 1189
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258 c 281 g 194 t 4 others
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Pred. No. 5.8e-28;
0; Mismatches 4
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/organism="Homo sapiens"
/db_xref="taxon:9606"
        /clone="IMAGE:1670196"
                                                                  59
                                                                  BASE COUNT
ORIGIN
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                                                                                                                                                                    1031 ccagctagogteteggecettgeegeceegtgeetgtatataegtgttetatagageetg 1090
                                         Gaps
                        0;
  10.6%; Score 280.6; DB 10; Length 435; 92.5%; Pred. No. 7.7e-28; ive 0; Mismatches 24; Indels 0;
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US-09-820-005-3_COPY_16200_18853 2654 1 tgtctaggccatagcttggc.....agctacttgggaggctgagg 2654 1472140 segs, 8248589755 residues IDENTITY_NUC Gapoxt 1.0 Title: Perfect score: Sequence: Scoring table: Searched:

2944280 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

Database :

GenEmbl:*

1. 9b.ba:*
2. 9b.hrg:*
4. 9b.om:*
5. 9b.ow:*
6. 9b.ph:*
7. 9b.ph:*
10. 9b.r:*
110. 9b.r:*
111. 9b.r:*
112. 9b.y:*
113. 9b.u:*
114. 9b.vi:*
115. em.bum:*
15. em.bum:*
16. em.cor:*
20. em.or:*
21. em.ov:*
22. em.or:*
23. em.ph:*
24. em.ph:*

em_ro:*
em_sts:*
em_un:*
em_un:*
em_v1:*
em_toj.hum:*
em_htgo.hum:*
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em_htgo.rod:*
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em_htgo.rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result Query No. Score Match Length DB ID 1 1934.4 72 9 230552 9 AC005098 2 1930.8 72.8 131359 9 AC004168 3 1930.8 72.8 131359 9 AC004168 4 1927.6 72.6 169604 9 AC083884 5 1735.2 65.4 124526 9 AC005080 6 1115.8 42.0 1730.2 9 AC005080 6 1115.2 87.1 1646 9 HS47P43S03 10 1025.4 39.7 1646 9 HS47P43S03 11 1025.4 39.7 1646 9 HS47P43S03 10 1027 38.7 1648 9 AC027219 11 1025.4 39.7 1648 9 HS47P40X03 12 532.8 20.1 149830 2 AC027219 13 537.6 19.5 149830 2 AC027219 14 284.4 10.7 5724 9 AC027219 15 229.6 8.7 17519 9 AC005227 16 22 229.6 8.7 17519 9 AC000352 20 229.6 8.7 17519 9 AC000352 21 229.6 8.7 17519 9 AC000352 22 223.6 8.4 158460 2 AC06752 22 223.6 8.4 158460 2 AC05524 23 223.6 8.4 158460 2 AC05524 24 223.8 8.4 100600 9 APWHYTBS22 25 222.4 8.6 13848 9 AC005524 26 221.2 8.3 138408 9 AC005524 27 221.2 8.3 138408 9 AC005524 28 219.6 8.3 134210 9 AC003564 29 221.2 8.3 134210 9 AC003564 29 221.2 8.3 134210 9 AC003564 217.4 8.2 160972 2 AC087848 217.4 8.2 183535 2 AC087848 217.4 8.2 183535 2 AC08366 2 41 216.8 8.2 202344 2 AC087841 2 21.2 8.3 134210 9 AC003566 2 41 216.8 8.2 202344 2 AC087848 2 217.2 8.3 134210 9 AC003566 2 41 216.8 8.2 202344 2 AC0878975 2 42 226.8 8.3 18489 9 AC085524 2 21.2 8.3 134210 9 AC003566 2 2 2 2 2 2 8 2 2 8 2 8 8 8 8 8 8 8 8 8	Description	AC005098 Homo :	1166 Homo s	3884 Homo s	05080 Homo sap.	1614 Hom	72 ношо ѕар	92405 Pap	10 Homo	1244 HOMO :	35 Homo sapi	219 Homo sa	AC027219 Homo sapi	מים מוויסוו במים	Human neut	Human 4	Homo sa	НОШО	3 Ното за	Ношо	7 Homo sa	Homo sa	ношо за	HOMO S	HOMO S	Нишап	Homo s	a compa	OMOH 670	63 Homo c	HOMO SA	52 HOMO SA	44 Homo sap	85 Homo sap	7 Homo	54 Homo sap.	348 Homo	5283 Homo	366 Ното sa	58720 Homo s	37119 Human	33375	975 Homo s
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ALIGNMENTS

SUMMARIES

AUTHORS

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                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (07-OCT-2000) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Jul 15, 2000 this sequence version replaced gi:3212893.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence of this clone was established as part of a mapping and sequencing collaboration between the NAGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgii.nih.gov/DIR/GTB/CHR7, send
                                                                                                                                                                                                                                                           Submitted (15-JUL-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA (5205) (bases 1 to 230552)
                                                                                                                         Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://www.nhgri.nih.gov/DIR/GTB/CHR7 , send
mailto:egreen@nhgri.nih.gov , or see http://genome.wustl.edu/gsc
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Actual start of this clone is at base position 1 of CTA-350L10;
actual end is at base position 230552 of CTA-350L10.
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                                                                                    Sequencing Center, Washington 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center project name: H_RG350L10
                                                      Direct Submission
Submitted (12-JUN-1998) Genome
University School of Medicine,
MO 63108, USA
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3 (bases 1 to 230552)
Waterston, R.H.
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Waterston, R.H.
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                                                         TITLE
JOURNAL
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JOURNAL
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The sequence CTA-350L10 from base position 222330 to 222775 is a GA rich region. The sequence is not exact but it is believed to be the best representation of this region. The region was sized by PCR from clone DNA at 650 bp. The region corresponds to restriction digest hindiii: band size 7685 in silico and 7756 real.

1. .230552 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="7"

Location/Qualifiers

source

FEATURES

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gccgcaacagcgtccgttttctgcagcagcgacgccgccaggcgcgggggggagcagaga
              GCCGCAACAGCGTCCGTTTTCTGCAGCAGCGACGCCGCCAGGCGCGCGGGACCGCAGA
                            ggcggaatcagagggagaggcggggactggaggcgggggcagaggaggaggcgctag
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                gtcccttagagataagagacaatcataaggggagatatcagagaaaatcgtaaggggagc
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Submitted (21-DEC-1999) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Feb 24, 1999 this sequence version replaced gi:3309099.
                                                                                                                                                                                  Euteleostomi;
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Missouri 63108,
                                 AC004883 131359 bp DNA PRI 21-DEC-1999
Homo sapiens PAC clone RP4-771P4 from 7q11.21-q11.23, complete
sequence.
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Submitted (12-JUN-1998) Genome Sequencing Center, Washington
Submitted (12-JUN-1998) Genome Sequencing Center, Washington
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Park Avenue, St. Louis,
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St. Louis,
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Sulston,J.E. and Waterston,R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
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Park Avenue, S
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MO 63108, USA
                                                                                                                                                                                                 Mammalia; Eutheria; Primates;
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Kalicki,J. and Laplant,Y.
The sequence of Homo sapiens
Unpublished
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Direct Submission
Submitted (18-WAR-1999) De
University, 4444 Forest Pa
6 (bases 1 to 131359)
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Submitted (20-FEB-1999)
University, 4444 Forest
5 (bases 1 to 131359)
                                                                                                           GI:4263746
                                                                                                                                                                                                                                                                                                                                                                              3 (bases 1 to 131359)
Waterston, R.H.
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4 (bases 1 to 131359)
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RESULT
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                                                                                                                          KEYWORDS
                                                                                                           VERSION
                                                                                                                                             SOURCE
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

Web site: http://genome.wustl.edu/gsc Contact: sapiens@watson.wustl.edu

Center code: WUGSC

Center project name: H_DJ0771P04

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington

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ERLSKVEKARQLREQVNDLFSRKFGEAIGMGFPVKVPYRKITINPGCVVVDGMPPGVS
FKAPSYLEISSMRRILDSAEFIKFTVIRPFPGLVINNQLVDQSESEGFVIQESAEPSQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Join(8610. 38708,10451. 10589,18436. 18570,19722. 1990
20081. 20109,24648. 24702,25874. 25917,30516. 30593,
49336. 343395,36373. 36429,38357. 38419,48276. 48386,
49719. 49784. 51970. 52153,53415. 53473,54953. 55024,
55992. 56175,57537. 57595,62939. 63010,64249. 64432,
65374. 65432,65828. 65902,67505. 67606,68515. 68580,
68758. 68941,70845. 770900,71574. 71654,72578. 72661,
73330. 73513,74993. 75021,76304. 76345,77444. 77485,
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                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="match to EST AA496950 (NID:92230271) aa42e07.s1"
8607. .8708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="GTF21"
/note="match to AF035737 (PID:g2827180); H_DJ0771P04.1"
                                                                                                                                                        /note="match to EST A1240430 (NID:93835827) qi14h03.x1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 gacceteacgggggaaaaggggetggacgegeetggeeggggtgtgggggetggeacggggg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 tgtctaggccatagcttggcagtgccgggggggggggtctctcagcctggcaggagaggcag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="general transcription factor 21"
/protein_id="AAD15419.1"
/db_xref="G1:4263747"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                         /note="match to EST Z39110 (NID:g561502)"
                                                                                    /note="match to EST T06057 (NID:9317206)" 8418. .8752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
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/gene="GTF2I"
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/gene="GTF21"
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697. .7001
rpt_family="Alu"
740. .6981
note="similar to EST A1346557 (NID:94083763) qp46d02.x1"
                                                                                                                                                                                  This clone was derived from human PAC library RPCI-4, prepared by pleter de Jong and coworkers at the Roswell Park Cancer Institute (http://Dacpac.med.buffalo.edu) using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994). The library is fro
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                                                                       http://www.nhgri.nih.gov/DIR/GTB/CHR7 , send
mailto:egreen@nhgri.nih.gov , or see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The clone sequenced to the left is RP5-1186P10. Actual start of this clone is at base position 1 of RP4-771P4; actual end is at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA525914 (NID:92267983) ni61e09.s1"
   For additional information
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note="match to EST N48220 (NID:g1189386) yv22d08.rl"
350. .4703
rpt_family="MER4-group"
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2043. .2408

Anote="match to EST H66847 (NID:g1025587) yr71c03.s1"

Anote="match to EST H68467 (NID:g1027207) yr83h06.r1"

2276. .2945
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/rpt_family="Alu"
3404 .3947 .
7405e="match to EST N39030 (NID:g1162237) yv22d08.s1"
3445 .3819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /rpt_family="Alu"
87. .549
/note="match to EST T90283 (NID:9718796) yd42c06.s1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="match to EST T82859 (NID:g711147) yd42b05.rl"
                                                                                                                                                                                                                                                                                                          one male donor.

The clone may be obtained either from Genome Systems, Inc. (http://www.genomesystems.com) or Research Genetics, Inc. (http://www.resgen.com); or from Pieter de Jong. VECTOR: pcyPAC2
NEIGHBORING SEQUENCE INFORMATION:
University Genome Sequencing Center. For addabout the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7 , send
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359. .6671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="7"
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/clone="RP4-771P4"
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1. .229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1. .131359
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/note="match to EST
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5005. .5265
/rpt_family="Alu"
5268. .5501
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/rpt_family="Alu"
7884. 7937
/rpt_family="L1"
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1649. 2069
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1111. .1407
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                                                                                                                                                        SOURCE INFORMATION:
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4

9 Gaps

107773

QQ	108854	GCCTCCGCCCAGGGTTA-TITCTAAGTTGAGGACA-GGAGGTTGTGAGTTCTG	108905
Οy	1261	ពពាធានភាពពាធានភាពពាធានការការការការការការការការការការការការការក	1320
qq	108906	CTGGGGGAAGTTGC	108920
Qγ	1321	<u>ពលពលពេលពេលពេលពេលពេលពេលពេលពេលពេលពេលពេលពេល</u>	1380
qq	108921	AAGAGCCGAGGTCTGGTTGCATGTTGCCCTGGTCTTGGCCAAGAACAGGTTTGCACAAGG	108980
Qy	1381	លលាលបានពេលពេលពេលពេលពេលពេលពេលពេលពេលពេលពេលពេលពេលព	1440
qq	108	CCAAGTTCAAGAGGAACTCCCGGTTTCCTGCTGACCGTTTGGTCAGAAACCACCTGCTTG	109040
QY	1441	<u> ពេលពេលពេលពេលពេលពេលពេលពេលពេលពេលពេលពេលពេលព</u>	1500
qq	109041	GACTCTGGCGGAAGAGTGCTGAAGATGGGTGCACACAGTGCAGCAGGGCAGCCCTGTCTC	109100
QY	1501	annanan	1560
qa	109101	ATGACAGGAGACAGGCTGCCGTCCAGGGTGTAGGAGTGACCTCATAGCTGGGATAAAAA	109160
Oy	1561	<u> </u>	1620
ΩD	109161	TATTATAACTT	109220
Qγ	1621	ចលាពេលពេលពេលពេលពេលពេលពេលពេលពេលពេលពេលពេលពេលព	1680
qq	109221	STGGGAGG	109280
Ωy	1681	นนนนนนนนนนนนนนนนนนนนนนนน	1740
qq	109281	ACCCCATCTCTACCAAAAATAAAAATTAGCTGGGCGTGGTGGCATGCAT	109340
Ωy	1741	00000000000000000000000000000000000000	1800
qa	109341	CAGCTACTGGGGAGGCTGAGGCATGAGAATCGCTTGAACCGGGGAGGCAGATGTTGCAGT	109400
Qy	1801		1860
qq	109401		109460
QY	1861	9ggcgtggtggcatgcatccacaatcccagctactgggga	1920
qq	109461	TAGCTGGCGTGGTGGCATG	
Ωy	1921	ctgaggcatgagaatcgcttgaaccgggggaggcagatgttgcagtgagccgagacggc	1980
OD	109521	GCTGAGGCATGAGAATCGCTTGAACCGGGGGGGGCAGATGTTGCAGTGAGCCGGCG	109580
QY	1981 109581	ccactgcactccagcctggactacagagcgagactctatctcaaaaaaaa	2040 109640
QY	2041	aaagtaacttaggtgcagggtgtcctctgttattcactgagaccgtgccccggttatgag	2100
QY Db	2101	gttgtaccagaaagcaagtattcactatgcacactattcaccgctcaccctagcattgaa	2160 109760
ÓΣ	216	agcctgtagcctgaaagcctttgctttgagggcaggtctttccccaaat	220
QQ	~	CCAGCCTGTAGCCTGAAAGCCTTTGCTTTGAGGGCAGGTCTTTCCCCAAAATGCAGAC	
QY	2221 109821	cgaaggtgcaaagtgaagctgccagtcttgcaaaagatgtaacttgtcacgaaggccacg 	2280 109880
Qy	228	agtggcagggagagctgtccccacatttgcggaagtggctatgtgaggacgggggggg	340
qq	109881	rggcagggaggrectacatitigggaaagiggciaigigaggacgggaggg	109940

Gaps

Indels

269;

Mismatches

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Conservative

Matches

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Submitted (20-JUL-2000) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
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Burian, D.M. and Roe, B.A.

Direct Submission

Submitted (21-FEB-1998) Department Of Chemistry And Biochemistry,

The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
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Submitted (01-JUL-2000) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Burian, D.M., Ren, Q., Meadows, S., Huang, E., Korenberg, J. and
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BAC Clone 239c10
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Jul 1, 2000 this sequence version replaced gi:8779478
Location/Qualifiers
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Ren,Q., Burlan,D., Huang,E.
Homo sapiens Chromosome 7 B2
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Length 275197;

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72.8%; 76.5%;

Best Local Similarity

Query Match

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Direct Submission
Submitted (04-OCT-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Materston, R.H.
Direct Submission

Submitted (23-MAY-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
on May 23, 2001 this sequence version replaced gi:13431264.
Center project name: H_NH0813J07.
                                                 2521 aggtgaatcacttgaggtcaggagttccagaccagcctggccaacatggtgaaacccat
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Homo sapiens clone RP11-813J7, complete sequence.
AC083884 G I:14190780
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/db_xref="taxon:9606"
/clone="RP11-813J7"
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Qy Db	1081 111847	atagagcctggcgtctggacgccgagggcagccccgaccctgtccagcgcgctcccgc	1140
Qy Db	11141	cacctcaataaatgttgcttggagtggaccgaggctctgcaggaatgcagggaggg	1200 111966
Óγ	1201	gotecgccccagggttattttctaagttgaggacagggaggttgtgagttctgnnn	1260
DP	111967	CGCCCCAGGGTTA-TTTCTAAGTTGAGGACA-GGAGGTTGTAGTTCT	112018
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qq	112034	AAGAGCCGAGGTCTGGTTGCATGTTGCCCTGGTCTTGGCCAAGAACAGGTTTGCACAAGG	112093
Qγ	, 1381	<u> </u>	1440
qq	112094	CCAAGTTCAAGAGGAACTCCCGGTTTCCTGCTGACCGTTTGGTCAGAAACCACCTGCTTG	112153
οy	, 1441	<u>ពពពពពពពពពពពពពពពពពពពពពពពពពពពពពពពពពពពព</u>	1500
qq	112154	GACTCTGGCGGAAGAGTGCTGAAGATGGGTGCACACAGTGCAGCAGGGCAGCCCTGTCTC	112213
QY	, 1501	<u>ពពពពពពពពពពពពពពពពពពពពពពពពពពពពពពពពពពពព</u>	1560
ΩD	112214	ATGACAGGAGACAGGCTGCCGTCCAGGGTGTAGGAGTGACCTCATAGCTGGGATAAAAA	112273
Ωy	, 1561	<u>ពតពពពពពពពពពពពពពពពពពពពពពពពពពពពពពពពពពពព</u>	1620
QQ	112274	TATATTATAACTTAGGTTCGGCGCGCGGTGGCTCACGCCTGTAACCCAGCACTTTGGGAAGA	112333
Qy	1621	ពពាជាពាជាជាជាជាជាជាជាជាជាជាជាជាជាជាជាជា	1680
Ω	112334	CCGAGGTGGGAGGATCCGTTGAGCCCAGGAGTTCGAGACCAGCCTGGCCAACATGGTGAA	112393
οy	1681	មានភាពពេលពេលពេលពេលពេលពេលពេលពេលពេលពេលពេលពេលពេល	1740
qa	112394	CCCCATCTCTACCAAAAATAT	112453
οy	1741	<u> </u>	1800
qu	112	CAGCTACTGGGGAGGCTGAGGCATGAGAATCGCTTGAACCGGGGAGGCAGATGTTGCAGT	112513
Οy	1801	<u> </u>	1860
Dβ	112514	GAGCCGAGACGGCGCCACTGGACTCCAGCCTGGACAACATGGTGAAACCCCATCTGTACC	112573
Ωŷ	, 1861	nnnnntaaaaattagctgggcgtggtggcatgcatccacaatcccagctactggggag	1920
qq	112574	AAAAATATAAAAATTAGCTGGGGGGGGGGGGGGGGGGGG	112633
QY	1921	gctgaggcatgagaatcgcttgaaccggggaggcagatgttgcagtgagccgagacggcg	1980
qq	112634	GCTGAGGCATGAAATCGCTTGAACCGGGGAGGCAGATGTTGCAGTGAGCCGAGACGC	112693
ΟY	19	ccactgcactccagcctggactacagagcgagactctatctcaaaaaaaa	2040
qq	11269	CCACTGCACTCCAGCCTGGACTACAGAGCGAGACTCTATCTCAAAAAAAA	112
Qy	20	aaagtaacttaggtgcagggtgtcctctgttattcactgagaccgtgcccggttatgag	2100
QQ	0 112754	AAAGTAACTTAGGTGCAGGGTGTCCTCTGTTATTCACTGAGACCGTGCCCGGTTAT	112813

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(bases 1 to 124526)
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                                                                                                                                                                                       COMMENT
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Submitted (12-MAY-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
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(bases 1 to 124526)
Sulston,J.E. and Waterston,R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
                                                              112994 AGTGGCAGGGAGAGCTGTCCCACATTTGCGGAAGTGGCTATGTGAGGACGGGGGAGGCGG 113053
                                                                                                                                                                                                                                                                                     Db 113054 GTCCCTTAGAGAT--GAGACAATCATAAGGGGAGATATCAGAGAAAATCGTAAGGGGAGC 113111
                                                                                                                                                                                                                                                                                                                                     Db 113172 ACTGGACGGCTGGGCACAGTGGCTTAGGCCTGTAATCCCAGCACTTTGGGAGGCTGACGC 113231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db 113232 GGGTGAATCACTTGAGGTCAGGAGTTCCAGACCAGCCTGGCCAACATGGTGAAACCCCAT 113291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens BAC clone CTA-269Pl3 from 7q11.2, complete sequence.
AC005080
                                                                                                                                                                                                     agtggcagggagagctgtcccacatttgcggaagtggctatgtgaggacgggggaggcgg 2340
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   gttgtaccagaaagcaagtattcactatgcacactattcaccgctcaccctaqcattgaa
                   gtcccttagagataagagacaatcataaggggagatatcagagaaaatcgtaaggggagc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2521 aggigaaicactigaggicaggagitccagaccagcciggccaacaiggigaaaccccat
                                                                                                                                                                                                                                                                                                                                                                                                         actggacggctgggcacagtggcttaggcctgtaatcccagcactttgggaggctgacgc
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The sequence of Homo sapiens BAC clone CTA-269P13
Unpublished
3 (bases 1 to 124526)
Waterston,R.H.
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Waterston, R.H.
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The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7, send mailto:egreen@nhgri.nih.gov , or see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                 63108, USA
                                                                              Genome Sequencing Center, Washington
dicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clone CTA-269P13 is from a release of the human BAC library CITB-HS-A. The library contains cloned DNA from human sperm. See. Shizuya et al., Proc. Natl. Acad. Sci. USA 89:8794-7 (1992); U-J. Kim et al., Genomics 34:213-8 (1996). The clone is available from Research Genetics, Inc. (http://www.resgen.com).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The clone sequenced to the left is RP4-754G14; the clone sequenced to the right is RP11-396K3. Actual start of this clone is at base position 1 of CTA-269P13; actual end is at base position 124526 of CTA-269P13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         not represent the entire insert of this
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="match to EST AA643257 (NID:92568475) nr61h09.s1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence was finished as follows unless otherwise noted:
                                                                                                                                                                                                                                                                                                  Submitted (02-001-2000) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri-65 On May 12, 2000 this sequence version replaced gi:3212911.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center: Washington University Genome Sequencing Center
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/note="match to EST D44965 (NID:g1572440)"
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Contact: saplens@watcson.wustl.edu
------ Summary Statistics
Center project name: H_RG269913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between neighboring data submissions.
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1. .138
Waterston, R. H.
Direct Submission
Submitted (12-JUN-2000) Genome
University School of Medicine,
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/map="7q11.2"
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Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center code: WUGSC
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                                                               /note="similar to EST AW236834 (NID:96569223) xm49f08.x1"
119. .483
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                                                                                                                                 146. 483
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306. .652
                                                                                                                                                                                                                                                                            EST AW177547 (NID:96443584)"
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             D44969 (NID:91572444)"
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712. 740
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899. 919
 42. .118
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complement(106. .396)
/db_xref="GI:3800554"
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1570. 1662
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1571. 1662
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1665. 1817
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1834. 1886
/rpt_family="L2"
1888. 2189
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2256. 2546
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4108. .4237
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3493. .3780
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247. .4422
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423. .4729
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107. .1395
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222. .5527
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8810. 9112

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        120

        Db
        122191
        GACCCTCACGGGGGAAAGGGCTGGACGCGCTGGCCGCGGTGTGGGGCTGGCACGGGGG
        122250

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                                                                                                                                                                                                                                                                                                                                                                54; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122431 AGACTACCGGCCCCTACTGCCCCCCACTTCCTCGGACCAGGGGTGCCCATCTGAGTCCC
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                                                                                                                                                                                                                                                                                                                                     Length 124526;
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                                                                                                                                                                                                                                                                                                                                    Score 1735.2;
Pred. No. 0;
0; Mismatches
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8194. .8466
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Best Local Similarity 74.7%;
Matches 1831; Conservative C
                  repeat_region
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ggcggaatcagagggagaggcgggactggaggcgggggcagaggaggagccagcc	ggggcggagcgatccctaagaggcggagtcagagggagaggcacaagcgggaggcggaggc 	cagagcgcggagcaggagttggagaccgcgggggggggg	gggccagtgtgcgggcggcgtctgactcggcccgctctctgcccgcagaggaggag	cggcagacgcagcgctctaaaccgcagccggcggtgcccccgcgggccgagcgccacccclc	atcctgaaccgctgcagcgagagcaccaagcggaagctggcgtctgccgtctgaggctgg 	agcgcagtccccagctagcgtctcggcccttgccgccccgtgcctgtatatacgtgttct	atagaycctggcgtctggacgccgaggcagccccgaccctgtccagcgctcccgc	caccctcaataaatgttgcttggagtggaccgaggctctgcaggaatgcagggaggg	ggctccgcccagggttattttctaagttgaggacagggaggttgtgagttctgnnnnn 	<u> </u>	CTGGGGGGAAGTTGC	ជា បានបានបានបានបានបានបានបានបានបានបានបានបានប	AAGAGCCGAGGTCTGGTTGCATGTTGCCCTGGTCTTGGCCAAGAACAGGTTTGCACAAGG	<u>០៣០០០០០០០០០០០០០០០០០០០០០០០០០០០០០០០០០០០</u>	⊢	numiniminiminiminiminiminiminiminiminimi	uu	ATGGCAGGAGACAGGCTGCCGTCCAGGGTGTAGGAGTGACCTCATAGCTGGGATAAAAAA	<u>ពតពពពពពពពពពពពពពពពពពពពពពពពពពពពពពពពពពពព</u>	TATATTATAACTTAGGTTCGGGCGCGGTGGCTCACGCCTGTAACCCAGCGCTTTGGGAGA	ពពាធពពពពពពពពពពពពពពពពពពពពពពពពពពពពពពពពពពព	CCGAGGTGGGAGGATCCGTTGAGCTCAGGAGTTCGAGACCAGCCTGGCCAACATGGTGAA	<u>ពពពពពពពពពពពពពពពពពពពពពពពពពពពពពពពពពពពព</u>	ACCCCATCTCTACCAAAAATATAAAAATTAGCTGGGCGTGGTGGCATGCAT	ពលពេលពេលពេលពេលពេលពេលពេលពេលពេលពេលពេលពេលពេ
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2 (bases 1 to 17302)
Chanock, S.J., Resler, J., Zhan, S., Hopkins, P., Lee, P., Barrett, D., Christensen, B.L., Curnutte, J.T. and Goerlach, A.
Direct Submission
Submitted (08-SFP-1999) Pediatric Oncology Branch, NCI,
NIH/10/13N240, Bethasda, MD 20892, USA
Location/Qualifiers
                                                                                                            Qy 1861 nnnnnntaaaaattaqctgggggtggtggcatgcatccacaatcccagctactggggag 1920 | DS 123938 AAAAATATAAAAATTAGCTGGGGGTGGTGGTGGATCCACCACCAGCTACTGGGGAG 123997

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        Db
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Db 124177 GTTGTACCAGAAAGCAAGTATTCACTATGCACACTATTCACCGCTCACCTAGCATTGAA 124236
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                     2101 gttgtaccagaaagcaagtattcactatgcacactattcaccgctcaccctagcattgaa 2160
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                                                                                                                                                                                                                                                                    AF184614 17302 bp DNA PRI HOMO sapiens p47-phox (NCF1) gene, complete cds. AF184614.1 GI:6983939
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LOCUS
DEFINITION
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JOURNAL
MEDLINE
PUBMED
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AUTHORS
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SLPTKISRCPHLLDFFKVRPDDLKLPTDNQTKKPETYLMPKDGKSTATDITGPIILQS
YRAIANYEKTSGSEMALSTGDVVEVVEKSESGWWFCQMKAKRGWIPASFLEPLDSPDE
TEDPEPNYAGEPYVAIKAYTAVEGDEVSLLEGEAVEVIHKLLDGWWVIRKDDVTGYFP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16530 TCCGCAACGTGCACAGCATCCACCAGCGGTCGCGGAAGCGCCTCAGCCAGGACGCCTATC 16589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16110 TGTCTAGGCCATAGCTTGGCAGTGCCGGGGGGGGCTCTCAGCCTGGCAGAGAGGCAG 16169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGGGGGCAGGGGCGCCCTCGGGCTTTGACGACGCCCCTCCCGCTGGGCCAGGTCGTCCA 16529
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                                                                                                                                                                                                 .7381,
.13259,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tgggggcaggggcgcctcgggctttgacgacgcccgtcccgctgggccaggtcgtcca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tccgcaacgcgcacagcatccaccagcggtcgcggaagcgcctcagccaggacgcctatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gccgcaacagcgtccgtttctgcagcagcgccgccagccggcggcggcggaccgcaga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 tgtctaggccatagcttggcagtgccgggggggggggctctcagcctggcaggagagaggcag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cggaaggaaagcggcgatgcccggggggctttgggggatgggcagtccaggggggctccccg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 17302;
                                                                                                                                                                              join(1961. .2032,5227. .5307,7041. .7116,7216. 8741. .8796,10900. .11022,11486. .11593,13142. 15946. .16050,16522. .16667,17002. .17123)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1115.8; DB 9;
Pred. No. 3.1e-209;
0; Mismatches 7;
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/db_xref="taxon:9606"
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                                                                                                                                               /product="p47-phox"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42.0%;
98.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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Gorlach, A., Lee, P.L., Roesler, J., Hopkins, P.J., Christensen, B., Green, E.D., Chanock, S.J. and Curnutte, J.T.
A p47-phox pseudogene carries the most common mutation causing p47-phox deficient chronic granulomatous disease
J. Clin. Invest. 100 (8), 1907-1918 (1997)
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GGGGCCAGTGTGCGGGGGGGGGGTCTGACTCGGCCCCGCTCTCTGCCCGCAGAGGA
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Mammalia, Euthería, Primates, Catarrhini, Hominidae;
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Chanock, S.J., Roesler, J., Hopkins, P.J., Lee,
Christensen, B., Curnutte, J.T. and Gorlach, A.
Genomic structure and the identification of
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Euteleostomi;
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1 (bases 1 to 18458)
Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W.,
Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., Dietrich,N.L.,
Bouffard,G.G., Legaspi,R., Lim,M., Maduro,Q.L., Maduro,V.B.,
Masiello,C., Mastrian,S.D., McCloskey,J.C., McDowell,J.Y.
Pearson,R., Prasad,A., Shevchenko,Y., Snyder,B., Stantripop,S.,
Thomas,J.W., Thomas,P.J., Touchman,J.W., Tsurgeon,C., Vogt,J.L.,
Walker,M.A., Wetherby,K.D., Zhang,L.-H. and Green,E.D.
                                                                                                                          GCCCCGGGAGCCCGCTCGGTGAGTGCAGC-GGAGAGGGCAAGGGCAAGCCCTAGGGG 1160
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                                                                            1581 GAGGGCAGTCCCCAGCTAGCGTCTCGGCCCTTGCCGCCCCGTGCCTGTACATACGTGTTC
                              geggeagacgeagegetetaaaccgeageeggeggtgeeceeegggegagegaeet
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center code: NISC
Web site: http://www.nisc.nih.gov
Contact: nisc_mouse@nhgri.nih.gov
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AC092405.1 GI:14595779
HTG; HTGS_PHASE1; HTGS_DRAFT.
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                                                                                        /map="772"..."
/map="772"..."
/map="772"..."
/mote="Human genomic Pl clone P43 is a p47-phox pseudogene which is defined by the presence of a GT deletion at the beginning of exon 2"
join(#60970.:s19. .7258,#60971..:1. .3348,1. .1619)
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Scripps Research Institute, 10550 N. Torrey Pines Rd.,
Jolla, CA 92037, USA
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                                                                                                                                                                                                                                                                                                                                                                            Score 1052.4; DB 9;
Pred. No. 1.5e-196;
0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                               239
                                                /organism="Homo sapiens"
                                                          /db_xref="taxon:9606"
/clone="Pl clone P43"
/chromosome="7"
               92037, USA
Location/Qualifiers
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/gene="NCF1"
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/gene="NCF1"
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/gene="NCF1"
/pseudo
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NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                    Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319
Consensus quality: 179816 bases at least Q40
Consensus quality: 179898 bases at least Q20
Consensus quality: 181141 bases at least Q20
Insert size: 168000; agarose-fp
Insert size: 184058; sum-of-contigs
Quality coverage: 10.52x in Q20 bases; agarose-fp
Quality coverage: 9.60x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13828: contig of 13828 bp in length 13928: gap of unknown length 31257: contig of 17329 bp in length 31357: gap of unknown length 42795: contig of 11438 bp in length 42895: gap of unknown length 61886: gap of unknown length 111639: contig of 18591 bp in length 111639: gap of unknown length 11139: gap of unknown length 11139: gap of unknown length 184558: contig of 72819 bp in length
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/db_xref="taxon:9555"
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/note="assembly_fragment"
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111740. .184558
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Project Information
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                                                                   ...- Summary Statistics
                      project name: ccx clone name: 170F23
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42896. .61486
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1. .13828
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                                                                                                       Db 138562 CAAGCGCGGGGCGCCCCCCCCAGGTGAGCGGGGTTCCCCGGGGCTGGGCGGGGTCGAGG 138503
                                                                                                                                          161 cagtccaggqqqqqqctccccqqaqagggqqcqacagaccgaaggctggtgaggggcgtgg 220
                                  Gaps
Length 184558
                                  296;
                                  Indels
DB 2;
                                  629;
                  Pred. No. 1.3e-194;
39.2%; Score 1039.6; 62.9%; Pred. No. 1.3e
                                  0; Mismatches
                                  Matches 1570; Conservative
                  Best Local Similarity
Query Match
                                                                                                                                           221
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DP QY

281 ttgtcccgccgggggtcgtgcagactaccggcccctactgcccccacttcctcggacca 340

761 gcacaagcgggaggcgaggccagagcggggggagttggagttggagacgcggcggggggg 820 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 11 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 11 137771 137472 GGCCTTGGTCAAGAACAGGTTTGCACAAGGCCAAGTGCAAGAGGAACTCCCGGTTTCCTG 137413 138382 TAG--GGCTCATCGAGTCCCTGGGGGCAGGGGAGCGCTCGGGCTTTGACGACGCCCTGTC 138325 138112 ---GGGGGGCGGGGCCAGAGGGCGGAATCAGAGGGAGAGGCGGACACTGGAGGCGGGGCC 138056 137590 CAGGGATGCCAGGAGGCCGGGCTCCGCCCCAGGGCTA-TATCTAAGTTAAGGACA-GGA 137533 138442 AGGGGCAGCAGAGGCAGAACCCTCACCGGGGAAAGGGGGCTGGACGCGCCTGGCCGGGTA 138383 1060 ggaagggcaagccctaggggggggggtcagcgggagaggcggggccagaggccaga 640 138324 CCGCTGGGCCAGGTCGTCCATCCGCAACGCGCACAGCATCCACCACCAGCGGCGGGAAGCG ggcgcggcggcgcgcagagagccccgggagcccgctcggtgagtgcagcgggagagagggca 138204 GGGGGGGGGGGGACGCAGAGCCCCGGGAAGCCCTCTCGGTGAGTGCAGCAGAAGGGGGCA gccagagagcgctgtgggcggggccagtgtgcggggcgggggggcgtctgactcggccccgct 137890 CTCTGCCCACAGAGGAGGAGCCGCAGACTCAGCGCTCTAAACCGCAGCCGCGGGGCCCCC 941 cgcggccgagcgccgacctcatcctgaaccgctgcagcgagagcaccaagcggaagctgg Db 137830 CGCGCCCAGCGCTGACCTCATCCTGAACCGCTGCAGCGAGAGCACCAAGCGAAGCTGG ctgtccagcgcgctcccgccacctcaataaatgttgcttggagtggaccgaggctctg Db 137650 crgrccagcgcgcgccacccaccaraaargrrgcrrgaagrgaaccgaggcrcrg 137532 GGTTGTGAGTTCTGCTGGGGGGAAGTTGCAAAGAGTCGAGGTCTGGTTGCATACTGCCCT 881 ctctgcccgcagaggaggagcggcagacgcagcgctctaaaccgcagccggcggtgccc ccgctggggccaggtcgtccatccgcaacgcgcacagcatccaccagcggtcgcggaagcg ggggtgcccatctgagtccctggggggcaggggcgccctcggggctttgacgacgcccgtc 138144 GGCCGGGTAAGCCCTAGGGGCGGAGTCAGCGG------401 821 521 581 1241 1121 1181 g Ωp qq qq qq g g qq g q ò ò q δ οy ŏ à ŏ ö ŏ δ ŏ δ Qy δ öλ δŻ

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Db 136577 GACAGAAGCTTTCAGAAAACCACTGGATGGCTGGGAATAGTGGCTCAGACCTGTAATCCC 136518
Db 137412 CTGACCGTTTGGTCAGAAACCACGGCTTGGACTCTGGCGGAAAAGTCCTGAAGATGGGT 137353
                                                                                                                                                                                                                                                  137232 CGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCAAGGTGGGAGGATCGCTTGAG 137173
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                                           Db 136672 ATGTGAGGATGGGGAGGCAGGTCCCTTAGAGATA-----
                                                                                Db 137352 GGCACAGTGCAGCGGGACAGCCCTGTCTCATGACAGGAGACAGGTTGCCATCCAGGGTA
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/note="Human genomic P1 clone P40 is a p47-phox pseudogene which is defined by the presence of a GT deletion at the
                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gorlach, A., Lee, P.L., Roesler, J., Chanock, S.J. and Curnutte, J.T. Direct Submission
Submitted (19-JUN-1996) Molecular and Experimental Medicine, The Scripps Research Institute, 10550 N. Torrey Pines Rd., CAL 1, La Jolla, CA 92037, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 told).
Corlach, A., Lee, P. L., Roesler, J., Hopkins, P. J., Christensen, B., Green, E. D., Chanock, S. J. and Curnutte, J. T.
A p47-phox pseudogene carries the most common mutation causing p47-phox deficient chronic granulomatous disease
J. Clin. Invest. 100 (8), 1907-1918 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chanock, S.J., Roesler, J., Hopkins, P.J., Lee, P.L., Bassett, D.T., Christensen, B., Curnutte, J.T. and Gorlach, A. Characterization of the genomic structure of the p47-phox gene
                                                                                                                                                                                                                                                                                               (NCF1) pseudogene, clone P40, exons 9-11
                                                                                                                                                                                                                                                                                07-JAN-1998
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2500 agcactttgggaggctgacgcaggtgaatcacttgaggtcaggagttccagaccagcctg
                                                                          gccaacatggtgaaaccccatctctacagaaaatataaaaattagccaggcgtggtggca
                                                                                                                                                                    Db 136397 CAAGCCTAGAATCCCAGCTACTCGGGAGGCTGAGG 136363
                                                                                                                                               2620 caagcctagaatcccagctacttgggaggctgagg 2654
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="P40"
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                                                                                                                    682 CGGAAGGAAAGCGGCGATGCCCGGGGGCTTTGGGGATGGGCAGTCCAGGGGGGGCTCCCCG 741
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                                  1 tgtctaggccatagcttggcagtgccggggggggggctctcagcctggcaggagagggag
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38.8%; Score 1028.6; DB 9 99.4%; Pred. No. 6.8e-192;
                 0; Mismatches
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        Similarity
        Best Local Sim
Matches 1053;
Query Match
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/note-"Human genomic Pl clone P41 is a p47-phox pseudogene which is defined by the presence of a GT deletion at the beginning of exon 2.".
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Gorlach,A., Lee,P.L., Roesler,J., Christensen,B., Chanock,S.J. and
Curnutte,J.T.
                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. [1 (bases 1 to 1619)]
Gorlach, A., Lee, P.L., Roesler, J., Hopkins, P.J., Christensen, B., Green, E.D., Chanock, S.J. and Curnutte, J.T.
A p47-phox pseudogene carries the most common mutation causing p47-phox - deficient chronic granulomatous disease J. Clin. Invest. 100 (8), 1907-1918 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (19-JUN-1996) Molecular and Experimental Medicine, The Scripps Research Institute, 10550 N. Torrey Pines Rd., CAL 1, La Jolla, CA 92037, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           p47-phox gene
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HS47P41S04 1619 bp DNA PRI 07-JAN Homo sapiens p47-phox pseudogene, clone P41, exons 9-11 U61244 US1:2754728
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                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 1619)
Chanock S.J., Roesler, J., Hopkins, P.J., Lee, P.
Christensen, B., Curnutte, J.T. and Gorlach, A.
Characterization of the genomic structure of Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1027; DB 9;
Pred. No. 1.4e-191;
0; Mismatches 5;
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/db_xref="taxon:9606"
/clone="P41"
/chromosome="7"
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1. 1619
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Matches 1051;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Homo sapiens p47-phox (NCF1) gene, exons 9-11, and complete cds.
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                                    gcagggcaagggtccttgtcgtgacggggggagccgcctcttgtcccgccgggggtcgtgc
                                            ggggggggagcgatccctaagaggcggagtcagagggagaggcacaagcgggaggcgagg
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SLPTKISRCPHILDFFKVRPDDLKLPTDNQTKRPETYLMPKDGKSTATDITGPIILOS
YRAIANYETGSEMALSTGDVVEVYEKSESOWWFCOMKARROWIPASFLEPLDSPDE
TEDPEPNYAGEPYVAIKATAVEGDEVSLLEGEAVEVIHKLLDGWYVIRKDDVTGYFP
SMYLOKSGOVYSQARQIKRGAPPRRSSIRWYHSIHQRSRKRLSQDAYRRNGYFLQO
RRRQARPGPQSPGSPLEERRQTQRSKPQPAVPPRPSADLIILNRCSESTKRKLASAV"
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                                                                                                                                                                                                   2 (bases 1 to 1645)
Chanock,S.J., Roesler,J., Hopkins,P., Lee,P., Bassett,D.T.,
Christensen,B., Curnutte,J.T. and Gorlach,A.
Genomic Structure and the Identification of Multiple Polymorphisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MGDTFIRHIALLGFEKRFVPSQHYVYMFLVKWQDLSEKVVYRRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pines Rd,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="NCF1"
join(U57833.1:<877. 8131,U57834.1:1. .3349,1. .1645)
/gene="NCF1"
join(U57833.1:877. .948,U57833.1:4143. .4223,
U57833.1:5957. 6032,U57833.1:6132. .6297,
U57833.1:7712,U57833.1:507. .629,U57834.1:1092.
U57834.1:7748. .2865,424. .528,1000. .1145,1480. .1601)
/gene="NCF1"
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U57833.1:5557. .6032,U57833.1:5612. .6297,
U57833.1:7657. .7712.U57834.1:507. .629,U57834.1:1092.
U57834.1:2748. .2865,424. .528,1000. .1145,1480. .1645)
             1 (bases 1 to 1645).
Corlach,A., Lee,P.L., Roesler,J., Hopkins,P.J., Christensen,B., Green,B.D., Chanock,S.J. and Curnutte,J.T.
A p47-phox pseudogene carries the most common mutation causing p47-phox deficient chronic granulomatous disease
J. Clin. Invest. 100 (8), 1907-1918 (1997)
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  Primates; Catarrhini; Hominidae;
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Gorlach, A., Roesler, J., Christensen, B., Chanock, S.J.
Curnutte, J.T.
                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (09-MAY-1996) P. Lee, Molecular and Expe
Medicine, Scripps Research Institute, 10550 North
La Jolla, CA 92037, USA
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Pred. No. 2.9e-191;
0; Mismatches 6; ]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="p47-phox"
/protein_id="AAB95193.1"
/db_xref="G1:2754713"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="Pl clone 42"
/map="7q11.23"
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1. .1645
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/gene="NCF1"
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/gene="NCF1"
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AC027219 149830 bp DNA HTG 03-MAR-2001 Homo sapiens clone RP11-729P19, *** SEQUENCING IN PROGRESS ***, 79 unordered pieces.

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NB., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Soon, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Soon, S., Baldwin, J., Barna, N., Barkien, V., Beda, F., Isandarier, B., Brown, A., Burkett, G., Lavoka, P., Colangelo, M., Collins, S., Dahano, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Domino, M., Doyle, M., Ferreira, P., Filzhugh, W., Gage, D., A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Domino, M., Doyle, M., Graham, L., Ferreira, P., Filzhugh, W., Gage, D., And, J., Gardya, S., Ginde, S., Goyette, M., Graham, L., Fardya, S., Ginde, S., Cooke, K., Macdonald, P., Marquis, N., Lanccque, K., Lancers, R., Lancers, T., Lanccque, K., Lancares, R., Mardad, C., Minoya, T., Miranda, C., Mlenga, V., Morrow, J., Y.T., Noylor, J., Norman, C. H., O'Connor, T., O'Connor, T., O'Connor, T., Olivar, T., M., Oliver, J., Peterson, K., Pierre, N., L., Santos, R., Schauer, S., Severy, P., Spencer, B., Savery, P., Spencer, B., Thoman, D., Ye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Ye, W., X., Wyman, D., Ye, W.J., Lev, H., Viel, R., Wollson, B., Wu, X., Wyman, D., Ye, W.J., Schauer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (28-2010) Whitehead Institute/MIT Center for Genome 320 Charles Street, Cambridge, MA 02141, USA 2001 this sequence version replaced gi:11610941.

11: Were identified using RepeatMasker:

12: A. & Green, P. (1996-1997)

13: Genome washington.edu/RM/RepeatMasker.html

14: Genome Center

15: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                 Metazoa, Chordata, Craniata; Vertebrata; Euteleostoml; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             i as it is available and the accession number will served.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ite: http://www-seq.wi.mit.edu
ct: sequence_submissions@genome.wi.mit.edu
----- Project Information
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3 GI:13184220
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contig or ____
pap of 100 bp
J: contig of 1088 bp in length
gap of 100 bp in length
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of 1029 bp in length
100 bp
of 820 bp in length
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1797 bp in length
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52901: contig of 1330 bp in length
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15862: gap of 100 bp
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717 bp in length
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6423: contig of 561 bp in length
23: gap of 100 bp
17467: contig of 944 bp in length
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53821: contig of 820 bp in length
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100 bp
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662 bp
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835: contig of 8
8835: gap of 100
9964: contig of 0
10784: contig of 8
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12415: contig of
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10885 11653: conti
11654 11753: gap of
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13333 14178: conti
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19983 21070: cont
21071 21170: gap of
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24482
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241 gcagggcaagggtccttgtcgtgacgggggcagccgcctcttgtcccgccggggggtcgtgc 300 cggaaggaaagcggcgatgcccgggggctttggggatggcagtccagggggggctccccg gagaggggacgacgaaggctggtgagggggggggaaaaccgcccaggctctgct tgtctaggccatagcttggcagtgccggggggggggggctctcagcctggcaggagagggag Length 149830; ; 97356: gap of 100 bp 10 Indels 80372: contig of 1993 bp in length 80472: gap of 100 bp 82236: contig of 1764 bp in length 82336: gap of 100 bp 84113: contig of 1777 bp in length 100 bp 1648 bp in length 73611: contig of 2361 bp in length 11: gap of 100 bp 75366: contig of 1655 bp in length 66: gap of 100 bp 78279: contig of 2813 bp in length 78279: gap of 100 bp 100 bp = 2102 bp in length 60655: gap of 100 bp 62781: contig of 2126 bp in length 03: gap of 100 bp 67667: contig of 1964 bp in length 86315: contig of 2102 bp in length 15: gap of 100 bp 89969: contig of 3554 bp in length 5: gap of 100 bp 7256: contig of 1730 bp in length 57801: contig of 2346 bp in length 100 bp 1489 bp in length 70: gap of 100 bp 65603: contig of 1133 bp in length 67: gap of 100 bp 69279: contig of 1512 bp in length contig of 906 bp in length Score 532.8; DB 2; Pred. No. 1.9e-95; p of 100 bp contig of 1771 bp in 100 bp 100 bp 0; Mismatches contig of contig of 106646 111055: gap of 111056 111155: gap of 986315: cord 901: gap of 59549: cont con ; gap of 71150: cr 50: 62881: gap of 64370: con 71250: gap of 95526: gap of gap of 92520: gap of 95426: con 20.1%; 99.6%; 60555: 55455: 59649: 73711: 75466: 86415: 100988: Conservative 78379: 65703: 84213: 9006 103743 64470: 69379: 97356: 57901 67767 Similarity 57802 57902 59550 59650 60556 60556 62782 62882 75467 78280 71151 71251 73612 73712 67668 67768 69280 69380 86416 89970 65604 65704 .03644 Query Match Best Local Simi Matches 534; 121 Н 181 Op qq ŏ Öλ δ Q δ Db δý

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Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.eughyRepeathwasker:
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Homo sapiens clone RP11-729P19, *** SEQUENCING IN PROGRESS ***, 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: sequence_submissions@genome.wi.mit.edu
------- Project Information
Center project name: L8346
Center clone name: 729_P_19
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens, clone RP11-729P19
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
NOTE: This is a 'working draft' sequence. It currently consists of 79 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9865 9964: gap of 100 bp 9665 9964: gap of 100 bp 9665 10784: contig of 820 bp in length 10785 10884: gap of 100 bp 10885 11553: contig of 769 bp in length 11554 11753: gap of 100 bp 12516 13232: contig of 762 bp in length 12516 13232: contig of 717 bp in length 1323 13322: gap of 100 bp 1333 14178 contig of 846 bp in length 1379 14289: gap of 100 bp 1479 14289: gap of 1484 bp in length 1479 14289: gap of 1484 bp in length 1479 14289: gap of 1484 bp in length 1479 1489
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24381: contig of 978 bp in length
81: gap of 100 bp
26183: contig of 1702 bp in length
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31434: contig of 1025 bp in length
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97356: gap of 100 bp 100888: contig of 3532 bp in length 100988: gap of 100 bp 103643: contig of 2655 bp in length 103743: gap of 100 bp 100 b
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73611: contig of 2361 bp in length
73711: gap of 100 bp
75366: contig of 1655 bp in length
75466: gap of 100 bp
78279: contig of 2813 bp in length
78379: gap of 100 bp
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80372: contig of 1993 bp in length
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44123: contig of 1025 bp in length
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25355: contig of 1134 bp in length
55: gap of 100 bp
57801: contig of 2346 bp in length
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contig of 1648 bp in length
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57281: contig of 2126 bp in length

181: gap of 100 bp

64370: contig of 1489 bp in length
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82236: contig of 1764 bp in length
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25: gap of 100 bp
38564: contig of 1239 bp
  35776: contig of 1242 bp
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ACO68263 57245 bp DNA HTG 30-APR-2000
Homo sapiens chromosome 4 clone RP11-225K6 map 4, LOW-PASS SEQUENCE
SAMPLING
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelęostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                       40341 ACACTATTCACCGCTCACCCTAGCATTGAAGCCCAGCCTGTAGCCTGAAAGCCTTTGCTTT 40282
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 4, clone RP11-225K6
                                                                                                                        DB 2;
                                                                                                                           19.5%; Score 517.6; DB 2 99.2%; Pred. No. 1.8e-92;
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Matches 520; Conservative
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16832: contig of
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McGarnan, K., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., O'Nell, D., Olivar, T.M., Olivar, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raynond, C., Riley, R., Rogov, P., Rothman, D., Stange-Thomann, N., Stonger, P., Spencer, B., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and Zody, M.

Birect Submission

AL Submitted (30-APR-2000) Whitehead Institute/MIT Center for Genome Submitted (30-APR-2000) Whitehead Institute/MIT Center for Genome All repeats were identified using RepeatMasker:

Smit, A.F. & Green, P. (1966-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                           Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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Center project name: L9566
Center clone name: 225_K_6
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75: gap of 100 bp
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SLPTKISRCPHLLDFFKVRPDDLKLPTDNQTKKPETYLMPKDGKSTÄTDITGPIILQT
TKATADVEKTSGSBMALSTGDVVEVVEKSEGGWWFCQMKARKGWIPASFLEPLDSPDE
TEDPEDNYAGEPYVAIKAYTAVEGDEVSLLEGEAVEVIHKLLDGWWYIRKDDVTGYFP
SWYLQKSGQDVSQAGYGIKKGAPPRRSSIRNAHSIHQRSRKRLSQDAYRRNSYFLQQ
RRRQARPGPQSPGSPLEEERQTQRSKPQPAVPRPSADLILNRCSESTKRKLASAV"
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TEIYEFHKTLKEMFPIEAGAINPENRIIPHLPAPKWFDGQRAAENRQGTLTEYCSTLM
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Gu, Y., Xu, Y., Souza, R.F., Nwariaku, F.E. and Terada, L.S.
Activation of c-Jun amino terminal kinase by a signaling oxidase
                                                                                                    /note="polymorphism; compared to sequence deposited in GenBank Accession Number AF330626"
/replace="c" 782
nnnnnnnnnnnnntaaaaattagctgggcgtggtggcatgcatcccacaatcccagctac 1913
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Homo sapiens adaptor protein p47phox (NCF1) mRNA, complete cds.
AF330627
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                                                                                                                                                                                                                                                                                                                                                                                                                      ttatgaggttgtaccagaaagcaagtattcactatgcacactattcaccgctcacctag
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/db_xxef="GI:13345798"
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1. .1340
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/organism="Homo sapiens"
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/product="adaptor
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/gene="NCF1"
/note="polymorphism; compared to sequence deposited in GenBank Accession Number AF330626"
/replace="g" 394 g 217 t
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1091 gcgtctggacgccgagggcagccccgaccctgtccagcgcggctcccgccacctcaat 1150

1151 aaatgttgcttggagtgga 1169

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1320 AAATGTTGCTTGGAGTGGA 1338

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Copyright (c) 1993 - 2000 Compugen Ltd.
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Rockville, Maryland 20850, USA Fax : (1) 301
Email : fliang@lifetech.com URL :
http://fullang@lifetech.com"
293 c 326 g 205 t 5 others
                                                           Score 914.6; DB 10; Length
Pred. No. 6.5e-128;
5; Mismatches 9; Indels
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//note=""Vector: proxysporr 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL:

http://tullengglb.invitrogen.com"
293 c 209 t 200 tchers
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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77 CGTCTCGGCCCCTTGCCGCCCCGTGCCTGTACATACGTGTTCTATAGAKCCTGGCGTCTGG
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Contact: Genoscope
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Email: segref@genoscope.cns.fr, Web : www
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3; Mismatches 43
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/db_xref="taxon:9606"
/clone="CSOD1087YH09"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CDNA clone CS0DI087YH09
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BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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Location/Qualifiers

FEATURES

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="csollo1874H09"
/clone_ilb="LTI_NFL06_PL2"
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/tissue_type="placenta"
/rote="weetor: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliangth.invitrogen.com"
/to the Property of th
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6; Mismatches 7;
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96.9%;
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/db_xref="taxon:9606"
/clone="csollo183xF12"
/clone_lib="LTI_NED06_PL2"
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/clone_lib="placenta"
/note="Vector: pCMVSPORT 6; Site_l: NotI; ist strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
Email: fliang@lifetech.com URL: http://fullength.invitrogen.com"

23 a 299 c 263 g 163 t 4 others
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Fill-length cDNA libraries and normalization
Contact: Genoscope
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Homo sapiens CDNA clone CSODI053YF12
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                                  : www.genoscope.cns.fr.
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                                                                                                                              Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqrefégenoscope.ons.fr, Web : www.
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 914)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full.length cDNA libraries and normalization
Unpublished (2001)
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AL574020 LTI_NFL006_PL2 Homo sapiens cDNA clone CSODI053YF12
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                    Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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/db_xref="taxon:9606"
                                                                                                                                                                        /clone="CS0DI053YF12"
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/issue_rype="B cells from Burkitt lymphoma"
//issue_rype="B cells from Burkitt lymphoma"
//note="Vector: pCMVSPORT 6: Site_1: Not1: 1st strand cDNA
was primed with a Not1-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Library was constructed by
Life Technologies. Contact: Contact: Contact: Diang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com
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BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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60.3%; Score 833.6; DB 10; Length 904;
Best Local Similarity 97.1%; Pred. No. 8.6e-116;
Matches 873; Conservative 1; Mismatches 11; Indels 14;
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
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/db_xref="taxon:9606"
/clone="CSODL012YG22"
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Catarrhini; Hominidae; Homo.
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Li,W.B., Gruber,C., Jessee,J. and Po
Full-length CDNA libraries and norma
Unpublished (2001)
Contact: Genoscope
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                www.genoscope.cns.
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                                                                                                                      /tissue_type="B cells from Burkitt lymphoma"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                             DB 10; Length
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Pred. No. 1.9e-114;
4; Mismatches 9;
               Web
                                                                                           /clone_lib="LTI_FL011_BC1"
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            segref@genoscope.cns.fr,
                                                                              /clone="CS0DG005YE05"
                         Location/Qualifiers
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Matches 906; Conserv
BP 191
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/note="Vector: pcMvSrORT 6; Site_1: NotI: 1st strand cDNA
was primed with a NotI-oligo(dT) primer: Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pcMvSrORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies.
a division of Invitrogen 9800 Medical Center Drive
Exevalla. Maryland 20850, USA Fax: (1) 301 610 8371
http://tulllength.invitrogen.com"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                      Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope_cns.fr, Web : www.genoscope.cns.fr.
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Li,W.B., Gruber.C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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Pred. No. 7.9e-113;
2; Mismatches 19;
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CDNA clone CS0DL001YL02
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
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//issue_rype="B cells from Burkitt lymphoma"
//note="Vector: pCMVSPORT 6; Site_1: Not1; 1st strand cDNA
was primed with a NotI-oligo(dr) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
Email: fliangelifetech.com URL:
http://fullength.invitrogen.com"
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   www.genoscope.cns.
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                                                       /clone="cs0bi001rb02"
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segref@genoscope.cns.fr, Web
Location/Qualifiers
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/db_xref="taxon:9606"
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 Email:
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                                              tacgtcgccatcaaggcctacactgctgtggaggggacgaggtgtccctgctcgagggt 787
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BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butelé
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/lab_host="DH10B"
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Pred. No. 3.1e-109;
6; Mismatches 8;
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/clone="CSODG007YL12"
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Best Local Similarity 98.3's
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CDNA clone CS0DL012YL03
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BP 191 91006 EVRX cedex - France
Email: segreféqenoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
ggtgaaatggcaggacctgtcggagaaggtggtctaccggcgcttcaccgagatctacga
                              caggatcatccccacctcccagctcccaagtggtttgacgggcagcgggccgagaa
                                                                   CCGCCAGGGCACACTTACCGAGTACTGCAGCACGCTCATGAGCCTGCCCACCAAGATCTC
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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/db_xref="taxon:9606"
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AL583335 LTI_NFL010_BC2 HG
Prime, mRNA Sequence.
AL583335 AL58335.1 GI:12952196
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Pred. No. 6.1e-109;
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/clone="CS0DL012YL03
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/fissue_type="B cells from Burkitt lymphoma"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
Email: filangelifetech.com URL:
http://fullength.invitrogen.com"

8 a 314 c 287 g 141 t 4 others
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Homo sapiens cDNA clone CS0DL008YK23
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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Pred. No. 4e-107;
                                                                                                                                                                                                                                                                                                                                                                                         /clone="CS0DL008YK23"
/clone_lib="LTI_NFL010_BC2"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
                                               cagoggtcgggaagogcctcagocaggacgc
                                                                                                                                mRNA
                                                                                                                              AL561678 954 bp
AL561678 LTI_NFL010_BC2
prime, mRNA sequence.`
AL561678
                                                                                                                                                                             AL561678.1 GI:12909344
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94.5%;
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JOURNAL
COMMENT
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                                                                                                      RESULT 1:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 851)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST 15-MAY-2001
602712304F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4852633 5'
BG758136
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                                                       731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
                                                                                                                                                                                                                                                                                     ccctggacagtcctgacgagacggaagacctgagcccaactatgcaggtgagccatacg
                                                                                                                                                                                                                                 gccagatcaagcggg-gggcgccgccagatcgtccatccgcaacgcgcacagcatc
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AUTHORS
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                                                                                               /tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: poTB7: Site_1: XhoI;
Site_2: EcoRI: CDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAGG(G). Size-selected >500bp
for average insert size 188b. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library." I others
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                                                                                                                                                                                                                                                                                          52.3%; Score 723.4; DB 11; 93.9%; Pred. No. 2.7e-99; iive 0; Mismatches 21; 1
 row: g column: 02
                                                /organism="Homo sapiens"
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/clone="IMAGE:4852633"
                                                                                     /clone_lib="NIH_MGC_48"
             stop: 841.
           High quality sequence stop: 8 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                    Conservative
                                    .851
Plate: LLCM1697
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/tissue_type="primary B-cells from tonsils (cell line)"
/tissue_type="primary B-cells from tonsils (cell line)"
/tab_host="blide (phage-resistant)"
/note="Organ: B-cells: Vector: poTB7; Site_1: XhoI;
Site_2: EcoR: CDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCACGGGG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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S NIH-MGC http://mgc.nci.nih.gov/.

National institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Emal: cgapbs-r@mail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboracory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BF974789 1070 bp mRNA EST 22-JAN-2001
602245439F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4336689
636 GCCGCCAGGCGCGC - CGGGACCGCAGAGCCCCGGGAGCCCGCTCGAGGAGGAGCGGCAGA
                                                          695 CGCAGCGCTCTAAACCGCAGCGGTGCCCCGC---GGCGAGCGCCGA-CTCATCCTGA
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Pred. No. 1e-98;
0; Mismatches 13; Indels 5:
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High quality sequence stop: 753.
Location/Qualifiers
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/organism="Homo sapiens"
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/clone="IMAGE:4336689"
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Best Local Similarity 97.7%;
Matches 772; Conservative (
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BF974789
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Query Match
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BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
                 ctaccggcgcttcaccgagatctacgagttccataaaaaccttaaaagaaatgttccctat
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
FM11-length cDNA libraries and normalization
Contact: Genoscope
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                                             /clone_lib="LTI_FL011_BC1"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Search completed: January 11, 2002, 11:34:22 Job time: 8814 sec

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Copyright (c) 1993 - 2000 Compugen Ltd.
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ALIGNMENTS

RESULT

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. DAT:

Human; antiinflammatory; protein coordinate data; chemical shift data; nuclear magnetic resonance; NMR; structural coordinate data; PX domain; reduced nicotinamide adenine diuncleotide phosphate; NADPH; NADPH oxidase; superoxide production; inflammatory disease, ds. (BIOM-) BIOMOLECULAR ENG RES INST. Sumimoto H; BP. DNA encoding human PX domain. 01-DEC-2000; 2000WO-JP08501. AAH45277 standard; DNA; 384 99JP-0346193. (first entry) Kohda D, Hiroaki H, WO200142453-A1 06-DEC-1999; Homo sapiens 07-SEP-2001 14-JUN-2001. AAH45277; AAH45277

Regulation of function of a protein containing a PX domain for controlling an inflammatory response to disease or trauma, comprises using nuclear magnetic resonance (NMR) chemical shift and structural

WPI; 2001-381679/40.

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present sequence is provided in a specification relating to the use
                                                                                                                        of chamical shift data from nuclear magnetic resonance (NNRS) and structural coordinate data of the PX domain of a protein to search for, evaluate, design and identify variant PX domain sequences for controlling the function of proteins containing the PX domain. It also relates to compounds promoting the binding of substances to the PX domain, and compounds inhibiting the binding of substances to the PX domain, The invention can be used in the identification of substances that can be used in the requiation of reduced nicotinamide adenine dinucleotide phosphate (NADPH) oxidase activity, which is involved in superoxide production in inflammatory response in disease or trauma.
                                                Page 185-186; 195pp; Japanese.
  coordinate data
                                                  Example 1;
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(HUMA-) HUMAN GENOME SCI INC

Rosen CA, Ruben SM; WPI; 2000-587534/55

99US-0124270.

12-MAR-1999;

08-MAR-2000; 2000WO-US05883

21-SEP-2000

Sequence 384 BP; 86 A; 127 C; 95 G; 76 T; 0 other;

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Human colon cancer antigen nucleotide sequence SEQ ID NO:448. BP. AAC98438 standard; cDNA; 425 (first entry) 09-MAR-2001 AAC98438 AAC98438
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Human; colon cancer; colon cancer antigen; diagnosis; detection; identification; cytostatic; cardioactive; neuroprotective; vulnerary; immunomodulatory; muscular; gynaecological; gastrointestinal; nephrotropic; antiinfective; antibacterial; gene therapy; wound; neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; renal disorder; infectious disease; cardiovascular disorder; ss.

■ WO200055351-A1. Homo sapiens

AAC97991 to AAC98763 encode the human colon cancer associated proteins, called human colon cancer antigens, given in AAB3234 to AAB54006. The human colon cancer antigens can have cytostatic, cardiactive, muscular; neuroprotective, immunomodulatory, gynaecological, gastrointestinal, vulnerary, nephrotropic, antiinfective and antibacterial activities, and can be used in gene therapy. The colon cancer antigen polynucleotides, proteins and antibodies to the proteins are useful for the prevention, treatment and diagnosis of colon disorders, such as colon cancer. The polynucleotides may be used in diagnostics and research, such as for chromosome identification, and as hybridisation probes. The proteins may also be used to prevent diseases such as neural disorders, immune system disorders, muscular disorders, reproductive disorders, immune system disorders, wounds, renal disorders, infectious diseases, and cardiovascular disorders. AAC98764 to AAC98772 and AAB54007 represent sequences used in the exemplification of the present Colon cancer associated gene sequences, referred to as colon cancer antigens, useful for the treatment, prevention, and diagnosis of colon 44 gacacetteatecgteacategecetgetgggetttgagaagegettegtaceagecag 103 Gaps 78; .DB 21; Length 425; Indels Sequence 425 BP; 103 A; 145 C; 102 G; 75 T; 0 other; Query Match 23.4%; Score 323.8; 'DB 21; Best Local Similarity 84.1%; Pred. No. 1.9e-59; Matches 423; Conservative 0; Mismatches 2; Claim 1; Page 930; 2104pp; English. disorders such as colon cancer P-PSDB; AAB53681 invention. q ōλ

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The present sequence is provided in a specification relating to the use of chemical shift data from nuclear magnetic resonance (NMR) and structural coordinate data of the PX domain of a protein to search for, evaluate, design and identify variant PX domain sequences for controlling the function of proteins containing the PX domain. It also relates to compounds promoting the binding of substances to the PX domain, and compounds inhibiting the binding of substances to the PX domain. The invention can be used in the identification of substances that can be used in the regulation of reduced nicotinamide adenine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; antiinflammatory; protein coordinate data; chemical shift data; nuclear magnetto resonance; NMR; structural coordinate data; Px domain; reduced nicotinamide adenine dinucleotide phosphate; NADPH; SH3 domain; NADPH oxidase; superoxide production; inflammatory disease; ds.
                                     343 aaagatggcaagagtaccgcgacagacatcaccggccccatcatcctgcagacgtaccgc 402
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Sequence 192 BP; 44 A; 50 C; 61 G; 37 T; 0 other;
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The invention relates to polynucleotides encoding novel human proteins or their active domains. The polypeptides, polynucleotides and antibodies raised against the polypeptides are used in a method of treatment of a mammal and prevention of disorders caused by the aberrant protein expression or activity. The polypeptides can be used as molecular weight markers, food supplements, and in antibody production. The polypeptides are used to identify compounds which bind to the polypeptides. Polynucleotides of the invention are used as probes and primers, for sequencing, for chromosome or gene mapping, in the polypeptides of recombinant proteins, and in generating anti-sense DNA or RNA and in gene therapy. Polypeptides of the invention can be used to target drugs to a tumour, in assays to determine biological activity, to target antibodies/elicit an immune response, to determine quantitative protein levels, as tissue markers, and to isolate receptors or ligands. Polypeptides of the invention may also be useful in treating platelet disorders, stem cell disorders, regenerating bouns, cartiage, tendon, ligament and/or nerve tissue, wound healing, treating burns, promoting the proliferation, differentiation and survival of stem cells, as a
                                                                                                                                                                                                                                                                                                                                                                                                                                  immunomodulatory, cytostatic; neuroprotective; vulnerary; nootropic; anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiaviral; antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic; thrombolytic; immunogen; antibody; gene therapy; neurological disorder; Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis; tissue regeneration; immune disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sclerosis, stroke, immune deficiencies resulting from bacterial, viral or fungal infection or from autoimmunity, cancer, allergy, asthma, graft-versus-host disease, eczema, haemophilia, thrombosis, anti-inflammatory diseases, nervous system disorders, and infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alzheimer's, Parkinson's and Huntington's diseases, amylotrophic lateral
                  novel protein; ss; Antianaemic; osteopathic; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for treating anti-inflammatory diseases,

    ggaaagacgacgtcacaggctacttcccgtccatgtacctgcaaaag

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nervous system disorders, and for regenerating bone and cartilage
                                                                                                                                                                                                                                                                                                                                                                      Human cDNA encoding a novel human protein #281.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 694-695; 894pp; English.
                                                                                                                                                                                                                                    AAS22715 standard; cDNA; 3195 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated polypeptides useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Liu C, Drmanac RT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-JAN-2000; 2000US-0491404.
                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                  872 tcagggcaagac 883
                                                                                                                           181 tcggggcaagac 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001-451939/48.
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                                                                                                                                                                                                                                                                                                                           24-OCT-2001
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                                                                                                                                                                                                                                                                                  AAS22715;
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Gaps

Score 154.8; DB 22; Length 192; Pred. No. 6.8e-24; 0; Mismatches 2; Indels 12;

Query Match 11.2%; Best Local Similarity 92.7%; Matches 178; Conservative

1 gagcccaactatgcaggtgagccatacgtcgccatcaaggcctacactgctgtggagggg 60 704 gagoccaactatgcaggtgagccatacgtcgccatcaaggcctacactgctgtggaggg

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AAF21398 standard; DNA; 7368
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                                                                                                                                                                                                                                                                                                                             goccaaagatggcaagagtaccgcgacagacatcaccggccccatcatcctgcagacgta 519
                                                                                                                                                                41 geccaagaaggaegtgaeaggtgeegaegeeacegeegageeeatgateetggaacagta 100
                                                                                                                                                                                                                       101 cgtggtggtgtccaactataagaagcaggagaactcggagctgagcctccaggccgggga 160
                                                                                                                                                                                                                                                                                161 ggtggtggatgtcatcgagaagaacgagagcggctggtggttcgtgagcacttctgagga 220
                                                                                                                                                                                                                                                                                                                                                                                                                                 754 tgtggagggggacgaggtgtccctgctcgagggtgaagctgttgaggtcattcacaagct 813
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                               ccgcgccattgccaactacgagaagacctcgggctccgagatggctctgtccacgggggga
                                                                                                                                                                                                                                                      cgtggtggaggtcgtagagaagagcgagactggttggtggttctgtcagatgaaagcaaa
                                                                                                                                                                                                                                                                                                                                                                        ccctgagccc----aactatgcaggtgagccatacgtcgccatcaaggcctacactgc
                                                                                                                                                                                                                                                                                                               gcgaggctggatcccagcgtccttcctcgagcccctggacagtcctgacgagacggaaga
                                                                                                       9
                                                                        Length 3195;
                                                                                                       Indels
The present sequence encodes a protein of the invention.
                             Seguence 3195 BP; 747 A; 964 C; 975 G; 509 T; 0 other;
                                                                        Score 99.8; DB 22;
Pred. No. 4.8e-12;
0; Mismatches 157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human cDNA encoding a novel human protein #45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tissue regeneration; immune disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAS22479 standard; cDNA; 5588 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tang YT, Liu C, Drmanac RT;
                                                                          7.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                       Best Local Similarity 56.3
Matches 210; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            814 cctggacggctgg 826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      401 tctggaaggctgg 413
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                                                                           Query Match
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                                                                                                                                    460
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The invention relates to polynucleotides encoding novel human proteins or their active domains. The polypeptides, polynucleotides and antibodies raised against the polypeptides are used in a method of treatment of a mammal and prevention of disorders caused by the aberrant protein expression or activity. The polypeptides can be used as motionation are used as probes and propertides are used to identify compounds which bind to the polypeptides. Polynucleotides of the invention are used as probes and princation of recombinant for chromosome or gene mapping, in the production of recombinant proteins, and in generating anti-sense DNA or NNA and in gene therapy. Polypeptides of the invention can be used to target drugs to a tumour, in assays to determine biological activity, to raise antibodies/elicit an immune response, to determine quantitative protein levels, as tissue markers, and to isolate receptors or ligands. Polypeptides of the invention may also be useful in treating platelet disorders, stem cell disorders, wound healing, treating burns, promoting the proliferation, differentiation and survival of stem cells, as a contraceptive, treating osteopoxosis and osteoarthritis, anaemia, and contraceptive, treating osteopoxosis and osteoarthritis, anaemia, and the proliment's stroke, immune deficiencies resulting from bacterial, viral or fundal infection or from autoimmunity, cancer, allergy, asthma, and any any and any any and any any and any any and any and any and any and any and any and any any and any any and any any and any and any and any and any and any any and any any and any any and any any any any and any and any any an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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d polypeptides useful for treating anti-inflammatory diseas system disorders, and for regenerating bone and cartilage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      583 catcaacacctctaagactggagaagtgtccaagagacgcaaggccca 630
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Best Local Similarity 56.6%; Pred. No. 1.7e-09;
Matches 163; Conservative 0; Mismatches 125;
                                                                                                                                                                                     English.
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                                                                                                                                                                               Claim 1; Page 240-245; 894pp;
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surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS; respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis; pulmonary hypertension; emphysema; pulmonary transplantation rejection; chronic obstructive pulmonary disease; pulmonary infection; bronchitis; respiratory obstruction; pulmonary obstruction; impeded respiration; cancer; ss.

Homo sapiens.

WO200062736-A2.

26-OCT-2000.

24-MAR-2000; 2000WO-US08020

99US-0127958. 06-APR-1999;

(UYEC-) UNIV EAST CAROLINA. (NYCE/) NYCE J W.

Nyce JW;

WPI; 2000-679539/66.

Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers and respiratory obstructions -

Disclosure; Page 1383-1385; 1592pp; English.

The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokine receptors, adeaion molecules and their receptors, central nervous system (CNS) and peripheral nervous and non-nervous system creceptors, defensine, growth factors, vasoactive peptides and receptors, defensines and malignancy associated proteins. The receptors, binding proteins and malignancy associated proteins. The antistre dispense oligonucleotides may be used in this way to treat disorders including proteins and may be used in this way to treat disorders including proteins and may be used in this way to treat disorders including proteins. including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary associated with a disease or allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAF18434 to AAF21543 represent human polynucleotide AAF18434 to AAF21543 represent human polynucleotide antisense oligonucleotides used in the exemplification of the present invention. fragments and

Sequence 7368 BP; 2018 A; 1656 C; 1890 G; 1804 T; 0 other;

. 0 Gaps 0; Length 7368; Indels 5.6%; Score 77.2; DB 21; 96.3%; Pred. No. 3.4e-07; tive 0; Mismatches 3; Query Match
Best Local Similarity yo..
*Ac 79; Conservative ò

110

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7347 gtgtacatgttcctggtgaaat 7368

AAA35276 ID AAA3

AAA35276 standard; DNA; 11651

AAA35276;

28-JUL-2000

(first entry)

Human adenosine receptor related polynucleotide 2nd SEQ ID NO:150.

antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway; lung disease; ischemic condition; pulmonary vasoconstriction; asthma; respiratory distress syndrome; pain; cystic fibrosis; emphysema; pulmonary hypertension; chronic obstructive pulmonary disease. COPD; Human; adenosine receptor; low adenosine antisense oligonucleotide; phosphorothioate; impaired respiration; inflammation; allergy; allergic disease; bronchoconstriction; inhibitor; antiinflammatory; cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

Homo sapiens.

WO200009525-A2.

24-FEB-2000

99WO-US17712. 03-AUG-1999;

98US-0095212.

03-AUG-1998;

(UYEC-) UNIV EAST CAROLINA.

Nyce JW;

WPI; 2000-205971/18.

New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstriction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia or cancers

Disclosure; Page 1298-1301; 1343pp; English.

The present invention describes a new composition comprising an antisense oligonuclectide (ON) with low adenosine (up to 15%), which targets nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antiinflammatchy, antiallergic, antiallergic, antiallergic, cytostatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation.

Impaired airways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma, impeded respirator, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, emphysema, chronic obstructive pulmonary hypertension, emphysema, chronic obstructive pulmonary and cancers such as leukaemias, lymphomas, carcinomas, and cancers which may metastasise to the lungs, including breast and prostate cancer. The reduction of the adenosine content of the observadenosine which activates adenosine receptors causing bronchoconstriction and inflammation. AAA33312 represent the nucleotide sequences given in the sequence listing from the present invention, which correspond to SEQ ID NO:1 to 2815, and then the last differ from the previously named sequences. SEQ ID NO:11 to 185, but the sequences (AAA32323 to AAA33992) are specifically claimed ONs from the present invention. NB. Sequences given in the disclosure of the present invention. NB. Sequences given in the disclosure of the present given in the sequence listing.

Sequence 11651 BP; 3079 A; 2635 C; 2989 G; 2948 T; 0 other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Low adenosine antisense oligonucleotide; phosphorothioate; allergy; human; airway disorder; bronchoconstriction; lung inflammation; surfactant depletion; respiratory; bronchodilator; antiinflammatory; immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic; respiratory obstruction; pulmonary obstruction; impeded respiration; surfactant hypoproduction; pulmonary vasoconstriction; asthma: RDS; respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis; pulmonary hypertension; emphysema; pulmonary transplantation rejection; chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oligonucleotides and compositions (1) comprising them. In the antisense oligonucleotides the A is replaced by a 'Universal' or alternative base. (1) can have respiratory, bronchodilator, antifilammatory, analgesito, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (1) can be used to down-regulate the expression and or activity of target polypeptides associated with lung/respiratory disorders and mailgnancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific engaymes, binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, adenosine receptors, bradykinin receptors, central
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers and respiratory obstructions -
                                                                                                   chemokine receptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peptide
                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                               Human low adenosine antisense oligonucleotide related sequence #2964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes low adenosine (A) content antisense
  Length 11651;
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                                          Indels
  Score 77.2; DB 21;
Pred. No. 3.7e-07;
                                        0; Mismatches
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                                                                                                                                                                              110 gtgtacatgttcctggtgaaat 131
5.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-MAR-2000; 2000WO-US08020.
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                                                                                                                                                                                                                                                                                            AAF21397 standard; DNA; 75
                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                        79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-679539/66
                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                           14-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer; ss
                                                                                                                                                                                                                                                                                                                                  AAF21397;
    Query Match
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                        Best Local
                                      Matches
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transmitters, defensins, growth factors, vasoactive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (sepecially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypoproduction rejection, inflections, bronchitis, and/or cancer. AAR18434 to AAR21843 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; adenosine receptor: low adenosine antisense oligonucleotide; phosphorothloate; impaired respiration; inflammation; allergy; allergic disease; bronchoconstriction; inhibitor; antiinflammatory; antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway; lung disease; ischaemic condition; pulmonary vasoconstriction; asthma; respiratory distress syndrome; pain; cystic fibrosis; emphysema; pulmonary hypertension; chronic obstructive pulmonary disease; COPD; cancer; leukaemia; lymphoma; carcinoma; metaatasis; ss.
                                                                                                                                                                                                                                                                                                                                                                      Human adenosine receptor related polynucleotide 2nd SEQ ID NO:149.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstriction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia or
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                                                                                                                                                                                                                                                                                                       Length 75;
                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                       DB 21; LA 3.7e-07;
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0
                                                                                                                                                                                                                                                      Sequence 75 BP; 15 A; 21 C; 19 G; 20 T; 0 other;
                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                         Score 75;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 1298; 1343pp; English
                                                                                                                                                                                                                                                                                     5.4%; Scor.
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA35275 standard; DNA; 75 BP.
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                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            tgttcctggtgaaat 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                             the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-205971/18
                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 75; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200009525-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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c inflammation. The ON can have antiinflammatory, antiallergies, and/or inflammation. The ON can have antiinflammatory, antiallergies, and/or antiasthmatic, cytostatic and analgasic activities. The compositions are useful for the treatment of diseases associated with inflammation, in mpaired airways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, emphysema, chronic obstructive fibrosis, pulmonary precension, emphysema, chronic obstructive conformed and cancers which may metastasise to the lungs, including breast and cancers which may metastasise to the lungs, including content of the ONs reduces side effects. The A-containing ONs break down with the created cancer. The reduction of the adenosine content of the obstruction and inflammation. AAA-33313 to AAA-33312 represent the nucleotide sequences given in the sequence listing from the present invention, which correspond to SEQ ID No:1 to 1887 but the sequences are also called SEQ ID No:1 to 1887, but the sequences (AAA-3232) to AAA-3323 to AAA-3324 to A
The present invention describes a new composition comprising an antisense oligonucleotide (ON) with low adenosine (up to 15%), which targets nucleic acids involved in bronchoconstriction, allergies, and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 75 BP; 15 A; 21 C; 19 G; 20 T; 0 other;
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Modulating the activity of I-kappaB kinases or cyclic nucleotide phosphodiesterases for the treatment of inflammatory disorders, autoimmune disorders (e.g. diabetes and Crohn's disease) and depression

Scudder KM, Bjorn SP, Thastrup O;

Arkhammar POG, Terry BR, WPI; 2000-399281/34.

P-PSDB; AAY84877

(BIOI-) BIOIMAGE AS

15-0CT-1998; 15-OCT-1998;

5-0CT-1998

99WO-DK00567. 98DK-0001321. 98DK-0001322. 98DK-0001323.

15-0CT-1999;

27-APR-2000

WO200023091-A2.

The specification describes a method for modulating the specific

Example 1; Page 84-89; 128pp; English.

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                      0; Indels
    DB 21; L 3.7e-07;
5.4%; Scor.
100.0%; Pred. No. J...
0; Mismatches
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                                                                                                                                      AAA14955 standard; DNA; 3201
                      Conservative
                                                                          117 tgttcctggtgaaat 131
                                                                                           tgttcctggtgaaat 75
             Local Similarity
nes 75; Conserv
                                                                                                                                                       AAA14955;
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                      Matches
                                                                                                                              AAA14955
                                                                                                                      RESULT
                                                      Db
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Length 75;

Query Match

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cyclic GMP; PDE3; PDE8; PDE8 splice variant; PDE4D; chronic broad inflammatory disease; chronic inflammation; airway disease; asthma; chronic bronchial hyper-reactivity; joint disorder; rheumatoid arthritis; pelvospondylitis; bowel disease; ulcerative colitis; Crohn's disease; autoimmune disease; diabetes mellitus type I; Hashimoto's thyroiditis; systemic lupus erythromatosus; myasthenia gravis; Grave's disease; immune thrombocytopenic purpura; acute respiratory distress syndrome; septic shock; depression; PDE1; PDE2; PDE6; PDE9; PDE10; jet lag; PDE5 splice variant; tension; erectile dysfunction; circadian rhythm;
                                                                                                                                           I-kappaB kinase; cyclic nucleotide phosphodiesterase; cyclic AMP;
                                                                                                         DNA encoding a PDE4D4-GFP fusion protein.
                                                                                                                                                                                                                                                                                                                           green fluorescent protein; GFP; ss.
                                                                    (first entry)
                                                                    21-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                 Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     effectiveness of I-kappaB kinases or cyclic modecide phosphodiesterases which have the ability to cleave cyclic AMP and/or GMP. This involves modulating the specific effectiveness of the cyclic nucleotide phosphodiesterase or I-kappaB kinase by modulating the spatial distribution within cells of the animal. If the cyclic nucleotide phosphodiesterase used is a PDE3, PDE7, PDE8 or a splice variant of PDE4 (such as PDE4D), the method is used to treat inflammatory diseases such as chronic inflammation (especially airway diseases such as asthma and chronic bronchial hyper-reactivity of non-asthma etlology, joint discorders such as wheumatoid arthritis and pelvospondylitis and bowel diseases such as ulcerative colitis and Crohn's disease), autoimmune diseases associated with inflammation (such as diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mellitus type I, systemic lupus erythromatosus, myasthenia gravis, thashimoto's thyroiditis, Grave's disease and immune thrombocytopenic purpura), disregulations of the immune system (such as acute respiratory distress syndrome (ARDS) and septic shock) and/or depression distress syndrome (ARDS) and septic shock) and/or depression. Alternatively, if the cyclic nucleotide phosphodiseterase is PDE1, PDE2, PDE6, PDE9, PDE10 or a splice variant of PDE5, the method is used to treat hypo or hypertension, erectile dysfunction, circadian rhythm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               resetting or jet lag. The present sequence encodes a fusion protein of PDE4D4 and green fluorescent protein (GFP), which is used in the course
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1015 ttttctgcagcagcgacgccaggcggcgggcgggaccgcagagcccgggagccggt 1074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   955 catccaccagoggtogoggaagogootcagocaggacgcotatogoogcaacagogtoog 1014
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87 caagcatctctggaggcacgagcaccagcaccagtacccgctccggcagccccagttccg 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 147 cetectycatececateaceaeetyceceegeegeegeegeeaeeetegeeeeageeceagee 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 207 ccaqtgiccgciacagccgccgccgccgccccccitgccgccgccccccgccgccgccgg 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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Best Local Similarity 52.3%; Pred. No. 0.048;
Matches 116; Conservative 0; Mismatches 106;
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11 RESULT

/product= "PDE4D-GFP fusion"

Location/Qualifiers

Aequorea victoria.

3201

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AAB54466. The human pancreatic cancer antigens, given in AAB54008 to AAB54466. The human pancreatic cancer antigens, given in AAB54008 to neuroprotective, noctropic, immunomodulatory, relaxant, contraceptive, or paracological, cardiant and antiinflammatory activities, and can be used in gene therapy. The polynucleotide and proteins can be used for preventing, treating, or ameliorating a medical condition or in assays for diagnosing a pathological condition or a susceptibility to one in a subject. Binding partners to the proteins and the activity of the proteins can be identified. The pancreatic cancer antigens can be used to detect, treat or prevent pancreatic disorders, especially cancer. Agonists and antagonists to the antigens can be used to design nucleic caid hybridisation probes that can be used in chromosome mapping, linkage and alternation and/or typing and a variety of forensic cancer antigen polynucleotides can be used to design nucleic cancer antigen polynucleotides can be used to design nucleic cancel alternation and/or typing and a variety of forensic cancel antigen polynucleotides the cancer antigen protection and/or typing and a variety of forensic cancel antigen polynucleotides the cancel antigen polynucleotides can be used to design nucleic cancel antigen polynucleotides can be variety of forensic cancel antigen partners to the protection and or typing and a variety of forensic cancel antigen polynucleotides the cancel antigen polynucleotides can be used to design antigen cancel antigen polynucleotides can be used to design and a variety of forensic cancel antigen polynucleotides can be used to design and a variety of forensic cancel antigen polynucleotides cancel antigen polynucleotides cancel antigen polynucleotides can be used to design and antagonist cancel antigen polynucleotides cancel antigen polynucleotides cancel cancel antigen polynucleotides cancel canc
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                                                                                                                                                                                                                                                                       Human; pancreas; pancreatic cancer; pancreatic cancer antigen; detection; daggnosis, identification; cytostatic; neuroprotective; noctropic; immunomodulatory; relaxant; contraceptive; gynaecological; antiinflammatory; cardiant; gene therapy; chromosome mapping; linkage analysis; issue identification; itssue typing; forensic; neural; immune system; muscular; reproductive; gastrointestinal; pulmonary; cardiovascular; renal; proliferative; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid that is a pancreatic cancer antiqen for preventing, ating, or ameliorating a medical condition, particular pancreatic ser, or for use in assays for diagnosing a pathological condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAC98773 to AAC99231 encode the human pancreatic cancer associated
                                                                                                                                                                                                            Human pancreatic cancer antigen nucleotide sequence SEQ ID NO:323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequences used in the exemplification of the present invention
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Pred. No. 0.057;
0; Mismatches 64; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 748; 1379pp; English.
                            AAC99095 standard; cDNA; 1214 BP
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                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-MAR-1999;
                                                                                                                                                      09-MAR-2001
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                                                                                       AAC99095;
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Best Local
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AAC99095
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of candidate compounds as agonists, for use as therapeutic agents -
The sequence encodes a human G-protein coupled receptor (GPCR), hRUP18 The endogenous and non-endogenous, constitutively activated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Endogenous and non-endogenous versions of human G-protein coupled receptors for direct identification of candidate compounds as agor
                                                                                                                                                                                    Human; G-protein coupled receptor; GPCR; hRUP18; agonist;
                                                                                                                                                               Human cDNA encoding G-protein coupled receptor, hRUP18.
                                        gtggaaaaaaaaaaaaaaaaaaaaaaaaaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inverse agonists or partial agonists
                                                                                                                                                                                                                                      Location/Qualifiers
1..1305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 43; Page 108; 159pp; English.
                                                                                                                                                                                                                                                           /*tag= a
/product= "hRUP18"
                                                                                                    ВР
                                                                                                                                                                                              inverse agonist; lung cancer; ss
                                                                                                  AAS07945 standard; cDNA; 1305
                                                                                                                                                                                                                                                                                                                                                                                                    99US-0171902.
2000US-0181749.
2000US-0189258.
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2000US-0196078.
2000US-0200419.
2000US-0203630.
2000US-0210741.
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99US-0166369.
99US-0171900.
99US-0171901.
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2000US-0195898.
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2000US-0235779
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                                                                                                                                            (first entry)
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                                                                                                                                            23-OCT-2001
                                                                                                                                                                                                                  Homo sapiens
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-NOV-1999;
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23-DEC-1999;
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versions of human G-protein coupled receptors (GPCR), are useful for direct identification of candidate compounds as receptor agonists, inverse agonists or partial agonists having applicability as therapeutic agents for treating diseases related to GPCR, e.g. lung cancer. Non-endogenous version of human GPCRs are also utilized in research settings and in vitro and in vivo system, incorporating GPCRs can be utilised to elucidate and understand the roles these receptors play in the human condition, both normal and diseased.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1082 gagcggcagacgcagcgctctaaaccgca----gccggcggtgcccccgcgcgcggcgc 1137
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                                                                                                                                                                                                                                                                                                                                                                                962 cagcggtcgcggaagcgcctcagccaggacgcctatcgccgcaacagcgtccgttttctg 1021
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                                                                                                                                                                                                                                                                                                                                                                                                                           585 CGGCGGCGGCGGCAGCGGCGAGGGGGAGTCCCCGCGCACCACGAAGGCCGGGGGCAGCGC 526
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                                                                                                                                                                                                                                                                                                                                      Gaps
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Y;
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                                                                                                                                                                                                                                                                                   DB 22; Length 1305; 0.2;
                                                                                                                                                                                                                                                                                                                                 0; Mismatches 140, Indels
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Kishimoto T, Kanzaki K, Yasuda S, Inoue
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                                                                                                                                                                                                               Sequence 1305 BP; 127 A; 500 C; 467 G; 211 T; 0 other;
                                                                                                                                                                                                                                                                                     Score 49;
Pred. No. 0
                                                                                                                                                                                                                                                                                        3.5%;
50.5%;
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2000JP-0101339.
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Best Local Similarity 50.5
Matches 147; Conservative
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Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
W vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
W vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
W anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
immunostimulant; thrombolytic; coagulant; vasotropic; antidlabetic;
W pyotensive; dermatological; immunosuppressive; antiinflammatory;
W antiviral; antibacterial; antifungal; antithemmatic; antithyroid;
antianaemic; gene therapy; cancer; proliferative disorder; hypertension;
w cardiovascular disease; diabates mellitus; hypothyroidism; SCID; AIDS;
cholesterol ester storage; systemic lupus erythematosus; infection;
severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
W allergy; aplastic anaemia; nocturnal heemoglobinutia; burn; wound;
W thrombosis; contraceptive; ss.
                                                                                                                                                                                                                                                                                                                                                    The invention relates to nine human guanosine triphosphate binding protein (G protein)-coupled receptors designated GRP48, GRP412, GPR416, GPR41, GPR
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                                                                     anticancer and nootropic drugs and in diagnosis of these diseases
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receptors and their expression products for screening potential
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Pred. No. 0.2;
0; Mismatches 140; Indels
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                                                                                                                                                                                                                Claim 1; Page 139-140; 170pp; Japanese.
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Best Local Similarity 50.5
Matches 147; Conservative
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AAC7446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; actiparatic; antiparkinsonian; nootropic; neuroprotective; costeopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coapulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; nypotensive; dermatological; immunosuppressive; antidiabetic; presence of or predisposition to, or preventing or treating the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy cetors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft valoat disease, cardiovascular disease, diabetes mellitus, hypothyroidism, cholesterol ester storage, systemic lupus acterial or fungal infection, malaria, automined dasorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, consultation antinflammatory disease; to enhance
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                                                                                                                                                                                                                      frame X,
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                                                                                                                                                                                                                  Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1316 BP; 325 A; 408 C; 395 G; 187 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         637 aaagcgaggctggatcccagcgtccttcctcga 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   453 taaggaaggtgggcccggccaccttcattga 485
                                                                                                                                                                                                                                                                         Claim 5; Page 1239-1240; 5507pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAX53491/c
ID AAX53491 standard; DNA; 114955
                                        31-MAR-1999; 99US-0127607.
02-APR-1999; 99US-0127636.
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
             31-MAR-2000; 2000WO-US08621
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 57.5
Matches 88; Conservative
                                                                                                                                           Shimkets RA, Leach M;
                                                                                                                (CURA-) CURAGEN CORP
                                                                                                                                                                        WPI; 2000-602362/57
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                                                       02-APR-1999;
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δλ
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The specification describes antisense oligonucleotides (AAX52869-X55271)

directed against at least 2 mRNAs selected from target genes, coding and non-coding regions of RNAs corresponding to target genes, coding and non-coding regions intriation codons, genomic flanking regions, intron-exon borders, the intriation codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-end and the juxta-section between coding and non-coding regions and all segments of RNAs encoding proteins associated with one or more diseases, conditions or MX55272-74. These multiple target oligonucleotides (specifically AAX5580-271) can be used for the antisense treatment of diseases and conditions. Typical diseases and conditions are those associated with impaired respiration and inflammation, including lung diseases, pulmonary vasoconstriction, and inflammation, allergic rhinitis, acute asthma, allergies, asthma, impeded inflammation, allergic rhinitis, acute asthma, allergies, asthma, impeded constructive pulmonary disease (COPD), and cancers such as leukemias, pulmonary disease (COPD), and cancers such as leukemias, parcreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma, carcinomas e.g. colon cancer, witchey cancer, melanomas, hepatic metastasized to the lungs, including breast and prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db 104986 GCGGCGCCCVGGCCVGNNHNNNSCGGCCCGGCCGCGCGCGCCCCVGGCCVGGCCVGCNNHNN 104927
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                                                                                                                                                                                                                  pulmonary hypertension; pulmonary vasoconstriction; emphysema;
chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
colon cancer; breast cancer; lung cancer; pancreatic cancer;
hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           642 gaggettggatececagegteetteetegageeeettggacagteetgaegagaeggaagaee 701
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Antisense oligonucleotide, multiple target; antisense treatment; impaired respiration; inflammation; lung disease; pulmonary vasoconstriction; inflammation, allergic rhinitis; acute asthma; allergy; asthma; impeded respiration; respiratory distress syndrome; pain; cystic fibrosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 114955;
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97US-0059160.
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Db 104326 GCGCCVGGCCNGCNNNNNSGGCCC 104299

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Š.

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Description	Human colorectal c	Human colorectal c	Human polynucleoti	Human polyamine-mo	Human neuroblastom	Human breast or ov	N. meningitidis pa	Human kinesin-like	Human breast or ov	Human lipolysis st	Genomic region con
ID	AAI57791	AAI57790	AA163970	AAF58067	AAF97861	AAI62640	AAA81655	AAC66548	AAI62714	AAX83427	AAX83426
DB	22	22	22	22	22	22	21	21	22	20	20
Query Match Length DB	32152	32204	10503	39198	13864	20444	1334	121162	7588	21721	22976
Query Match	10.9	10.8	10.3	10.2	10.1	10.1	10.0	9.9	9.6	8.6	9.8
Score	358.4	356.4	339.8	337.4	333.2	332.6	329.8	326.6	324	323.8	323.8
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2000US-0217496.
2000US-0218290.
2000US-0220963.
2000US-0220964.
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20000S - 024 6475

20000S - 024 6476

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20000S - 025 1679

20000S - 025 1686

2000S - 025 1686

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2001US-0259678
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(HUMA-) HUMAN GENOME SCI INC

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-457727/49

Isolated polypeptide for treating, preventing and/or prognosing disorders related to the colon and rectum including colorectal cancers and also for testing and detection e.g. diagnosis -

Disclosure; SEQ ID NO: 328; 522pp + Sequence Listing; English

The present invention provides the protein and coding sequences of a number of colorectal cancer antigens. These are shown in AAI57547-AAI57619 and AAM38569-AAM38641. These can be used in the diagnosis, prevention and treatment of cancer of the colon and/or rectum. The present sequence is a colorectal cancer antigen genomic sequence. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

9229 T; 0 other; Sequence 32152 BP; 8332 A; 7335 C; 7256 G;

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2000US - 0.205515
2000US - 0.204467
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2000US - 0.215136
2000US - 0.22514
2000US - 0.23141
2000US - 0.23149
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2000US - 0.23149
2000US - 0.23149
2000US - 0.23149
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14-AUG-2000;
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                                             1;
                                                                   3030 ccaccgtgcctggcctgtttttt.........gaaatgaggtc 3064
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                                             Gaps
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                                                                                                                                                                                                                                                                                                      2970 cctgacctcaagtgatccacccacctgggcctcccaaagtgctgggattacaggcatgag
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                Length 32152;
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                           .4e-82;
les 111; Indels
               22;
               DB
                                          0; Mismatches
               Score 358.4;
Pred. No. 2.4
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2000US-0180628.
2000US-0184664.
2000US-0186350.
2000US-018974.
2000US-0190076.
             Query Match 10.9%;
Best Local Similarity 77.2%;
Matches 460; Conservative
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18-APR-2000;
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The present invention provides the protein and coding sequences of a number of colorectal cancer antigens. These are shown in AALIST61-AALIST619 and AAM38569-AAM38641. These can be used in the diagnosis, prevention and treatment of cancer of the colon and/or rectum.
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                                                                                  2000US-0241808.
2000US-0241809.
2000US-0241826.
2000US-0244617.
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The present sequence is a colorectal cancer antigen genomic sequence. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                       11614 TITITAGTAGAAACAGGGTTTCACCATGTTGGCCAGGCTGGTCTCAAACACCTGATCTCA 11555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTTAGTAGAGACGGGGTCTCAACACATTGGCCAGGCTGGTCTTGAACTCCTGACCTCAAG 11255
                                                                                                                                                                                                                                                         agiggicacgaicteageteactgeaaceteegeetteeaggiteaactggiteteetgee 2859
                                                                                                                                                                                           2740 tttttgttatttttttgtgtttttgagacagagtcttgatctgttgcccaggccagagtgc 2799
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                                                                                                                                            Best Local Similarity 77.6
Matches 455; Conservative
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Barash SC, Ruben SM;
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                                                                                                                  The invention relates to human polynucleotides (AA163803-AA164012) and the encoded proteins (AAM43497-AAM4360) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes were isolated from a range of human tissues disclosed in the genes were isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists or useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, come, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, c.cohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative collis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 10503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29;
                                                                                                                                                                                                                                                                                                                                                                                                        Note: The sequence data for this patent did not form part of printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                        ID NO 342; 664pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10503 BP; 3137 A; 2004 C; 2211 G; 3151 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.3%; Score 339.8; DB 22; Length 75.5%; Pred. No. 9.7e-78; Live 0; Mismatches 117; Indels
                                  New isolated nucleic acids and polypeptides, useful for treating and/or preventing human diseases and disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gtgcctggcctgttttttgaaatgaggt-----
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2001-488781/53
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The present invention provides the protein, coding and genomic sequences of the human polyamine-modulated factor-1 protein (PMF-1). The sequences, and antibodies and analogues of the protein, are useful in the treatment of cancer, via regulation of the spermidlne/spermine NI-acetyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2734 tretetttttttgttattttttttgtgtttttgagacagagtettgatettgttgeecaggeea 2793
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid encoding human polyamine-modulated frregulating a polyamine-modulated factor-1-responsive, polyamine-dependent gene in a cancerous cell
                                                                                                                                                                                                                                                       Human; polyamine-modulated factor-1; PMF-1; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SSAT) gene. The present sequence is the PMF-1 gene.
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                                                                                                                                                                                                         PMF-1 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE
                                                                                                                                                                                                      polyamine-modulated factor-1
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                                             AAF58067 standard; DNA; 39198
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                                                                                                                                                                                                                                                                                                            Homo sapiens
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RESULT
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DB 22; Length 13864;

Query Match

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Human neuroblastoma cell line NB-1 1p36 nucleotide sequence SEQ ID NO:75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a homozygosity deletion domain co-existing in the 36-position of the first chromosome short arm (1p36) in human neuroblastoma. Also described are base sequences from the 1p36 position of human neuroblastoma cell lines (NB-1 and MASS-NB-SCH-1), which are tumour suppressor genes in human neuroblastoma. The genes are tumour markers and reagents in studying mechanism of tumour body formation, and gene diagnosis of tumours as well as in developing anti-cancer drugs. AAF977787 to AAF97829 represent PCR primers used in the exemplification of the present invention, and AAF97830 to AAF97841 represent sequences given in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human 1p36 homozygosity deletion domain from the 36-position of first chromosome short arm in human neuroblastoma cell lines, applicable e.g. in gene diagnosis of tumors as well as in developing anti-cancer drugs
                                                       3191
                                                                                                                                                                                                                                                                                                                                                                                         Human; chromosome 1; 1p36; neuroblastoma cell line; NB-1; anticancer; tumour suppressor; human 1p36 homozygosity deletion domain; tumour;
4846 ctcagccttccaagttgctgggactacaggcccgcaccacgccggctaatttttat
                                                       ctcagcccttgagtagctggggctacaggcgcacaccaccatgcctggctagtttttaa
                                                                                                                4906 attitiggtagaggagggtttcaccatgttgtccagtctggttgcaaactcctgggctc
                                                                                                                                                                      Example 8; Page 143-149; 226pp; Japanese.
                                                                                                                                                                                                                                                                          ВР
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                                                                                                                                                                                                                                                                          DNA; 13864
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-AUG-2000; 2000WO-JP05930
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Sequence 13864 BP; 3536 A; 3244 C; 3560 G; 3524 T; 0 other;

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                                   agacctitctcttttttgttatttttttgtgttttgagacagagtcttgatctgttgccc 2787
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                                                                                                                                                                                                                                                                                                              or ovarian antigen genomic DNA SEQ ID NO: 290
                  Indels
Score 333.2; DB 22;
Pred. No. 5.7e-76;
); Mismatches 118;
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2000US-0180628.
2000US-0184664.
2000US-0186350.
2000US-018974.
2000US-0198123.
10.1%;
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13-OCT-2000;
20-OCT-2000;
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The present invention provides the protein and coding sequences of a number of ovarian and breast antigens. These are shown in AAIG2467-AAIG2572 and AAW42240-AAW42345. The sequences can be used in the diagnosis, prevention and treatment of breast and ovarian cancers, and their metastasses. The present sequence is a genomic sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acids and polypeptides, useful for diagnosing, treating and/or preventing human diseases and disorders
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                                2000US - 024 I 787

2000US - 024 I 1808

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2000US - 024 6474

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                                                                                                           2742 tttgttatttttttgtgttttgagacagagtcttgatctgttgcccaggccagagtgcag 2801
                                                                                                                    2981 gigaticeacceacitgggceteceaaagigetigggatiaeaggeaigageeacegigeet 3040
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                                                                       20444;
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                                             other
                                                                       Length
                                                                      Score 332.6; DB 22; Length
Pred. No. 9.7e-76;
0; Mismatches 114; Indels
        Note: The sequence data for this patent did not form specification, but was obtained in electronic format at ftp.wipo.int/pub/published_pct_sequences.
                                            Sequence 20444 BP; 6413 A; 3836 C; 4185 G; 6010 T; 0
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Best Local Similarity 77.8%;
Matches 444; Conservative
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AAA81452 represent Neisseria meningitidis MenB polynuclectide ORF sequences, which are all used in the exemplification of the present inventor. The nucleic acid sequences, protein sequences, and antibodies against them, can be used in the manufacture of a composition. The composition can be used as a medicament (or in the manufacture of a composition or be used as a medicament (or in the manufacture of a medicament) for treating, preventing or diagnosing infection due to medicament) for treating, preventing or diagnosing infection due to neisserial bacteria. For example, some of the identification due too Noisserial bacteria. For example, some of the identification of sequences and and and an advantage of an antipacture of an antipacture of an antipacture. The particularly organism-specific probes. Attempts to make efficacious meningococcus B vaccines have failed mainly due to antigen tolerance. Multivalent vaccines have also been tried but none have successfully overcome antigenic variability. The provision of further, complete sequences may provide an opportunity to identify secreted or surface exposed proteins that may be presumed targets for the immune system and which are not antigenically variable or at least more conserved than
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                                                                                                                                                                                                                                                                                              Scarlato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated nucleotide sequences of Neisseria meningitidis which can be used in the diagnosis and treatment of N. meningitidis infection and other Neisserial infections, for example, N.gonorrhoea -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes methods of obtaining immunogenic proteins from Neisseria genomic sequences. AAA81453 to AAA82414 represent specifically claimed Neisseria meningitidis genomic DNA sequences; AAA81260 to AAA81303 and AAA825620 to AAB2563 rapresent Neisseria DNA sequences and their corresponding proteins; AAA81254 AAA81259 and AAA81304 to AAA81321 represent PCR primers used in the isolation of Neisseria meningitidis DNA sequences; and AAA81322 to
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Pred. No. 1.5e-75;
1; Mismatches 108; Indels 14;
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Ratti G, Scarselli M,
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Best Local Similarity 78.1°
Matches 438; Conservative
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R, Pizza M;
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24-FEB-2000;
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                                                                                                                                                     Human; kinesin-like protein; HKLP; KIF1; cell division; cancer;
intracellular transport; neurological disorder; infertility;
biallelic marker; spontaneous abortion; neonatal chromosome disorder;
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                                                                                        1035 ACAGICICACITITACCCAGGITGGGIGCAGGIGGTGATCATGGCITATTGCAGCC
                                       tcaacctcccaggcccaagtgatctcctgcctcagccccttgagtagctgggggtacag
                                                               975 TCGACCTCCTGGGCTCAAGTGATCCTCCCACCTCAGCCTCCCAAGTAGCTGAGACCTCAG
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Length 121162; 27;

9.9%; Score 326.6; DB 21; Length 76.2%; Pred. No. 7.9e-74; Live 0; Mismatches 114; Indels

Best Local Similarity 76.2 Matches 452; Conservative

Query Match

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Human; breast antigen; ovarian antigen; cancer; metastasis; gene therapy;
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New isolated nucleic acids and polypeptides, useful for diagnosing, treating and/or preventing human diseases and disorders -
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invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO

The present invention provides the protein and coding sequences of a number of ovarian and breast antigens. These are shown in AAM16240-AAM42340. The sequences can be used in t diagnosis, prevention and treatment of breast and ovarian cancers, and their metastases. The present sequence is a genomic sequence of the

Disclosure; SEQ ID NO: 364; 520pp + Sequence Listing; English.

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                                                                                              Score 324; DB 22; Dred. No. 1.1e-73; 0; Mismatches 120;
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at ftp.wipo.int/pub/published_pct_sequences
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Local Similarity 75.0%;
des 444; Conservative
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This sequence represents the human lipolysis stimulated receptor (LSR) genomic sequence. The novel LSR binds lipoproteins in presence of free fatty acids (FRA) and binds cytokines in absence of FRA. The nucleic acid and its fragments are used as probes and primers for detection and/or amplification of LSR genes; for production of recombinant LSR; for detecting allells variants, mutations, deletions, loss of heterozygosity and genetic abnormalities in the gene. LSR, recombinant cells and transgenic animals are used to screen for chemical interacting with LSR, also to study expression and activity of LSR and its interactions. The chemicals, and leptin, are used to modulate the number of LSR in a cell, its recycling rate and/or specificity of receptor activity, particularly of reducing the level of leptin, lipoproteins, chylomicrons and/or triglycerides. The chemicals are thus useful for treating eating disorders, particularly obesity (and related diseases such as atherosclevosis, hypertension and diabetes) or anorexia,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lipolysis stimulated receptor involved in leptin metabolism -controlling its activity for treatment of obesity, anorexia or
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Pred. No. 1.9e-73;
0; Mismatches 112; Indels
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Best Local Similarity 75.5%;
Matches 457; Conservative 0
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98WO-IB01257
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                                                                                                                                                                                                                                                                                                                       Human: lipolysis stimulated receptor; LSR; lipoprotein; free fatty acid; cytokine; probe; primer; amplification; hybridisation; detection; leptin; allele; variant; mutation; deletion; loss of heterozygosity; chylomicron; transgenic animal; gene expression; triglyceride; eating disorder; obesity; atheromatosis; atherosclerosis; hypertension; diabetes;
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                                                                                                                                                                                                                                                                                               Genomic region containing human lipolysis stimulated receptor gene.
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           5940 GGTCTCAAACTCCTAGGCTCAAGTGATCCTCCTGCCTTGGCCTCCCAAAGTGCTGAAATT
                                                               3232 aatcttgaactcctcggcttaagcaaccctctggtctcagcctcccacagtgctaggatt
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(INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
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                                                                                                                                                                                          aactectgaceteaagtgatecaceceaectgggeeteceaaagtgetgggattacaggea 3025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6117 CAGGCTGGAATGCAGTGGCACGATGATGACTCAAGCCTTGACCTCTCAAGCCCAAG 6058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gct-----agtttttaaaattttgtggagatgaggttcactatgttgtccaggct 3231
                                                                                    2726 caagacetttettettttttgttattttttgtgtttttgagacagagtettgatetggttge 2785
                                                                                                                                                                                                                                                         ctggttctcctgcctcagcctccagagtagttgggattacaggtgcccaccaccacgcct 2905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATCTCCTGACCTCAGGTGATCCACCCACCTCGGCCTCCCAAAGTGCTGGGATTACAGGTG 6178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------ 3059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6177 TGAGCCACTGCGCCCAGCCTATTTTCTTTTCAAAGACAGGGTCTCACTCTGTCACC 6118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tgatectectgeeteageceettgagtagetgggggetacagggegeacaccatgeetg 3179
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                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lipolysis stimulated receptor; LSR; chromosome 19q13.1; human; single nucleotide polymorphism; biallelic marker; obesity; atherosclerosis; insulin resistance; hypertension; hyperlipidemia; hypertriglyceridemia; cardiovascular disease; microangiopathy;
                                                                                                                                                                                                                                                                             ggctaatttttgtatttttagtagagacagggtttcaccatgttggccagactggtctca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aggtctggagtgcagtggtgcgatcatagttcactgcagcctcaacctcccaggcccaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCTAATTTTTAAATTTTTAAAATTTTTGTAGACATGGGGTCTCATTTTGTTGTCCAGGCT
Length 22976;
                                           36;
Score 323.8; DB 20;
Pred. No. 2e-73;
0; Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        syndrome X; diagnosis; therapy; genotyping; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human lipolysis stimulated receptor (LSR) gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tgagccaccgtgcctggcttt------
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1..2000
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9.88;
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  Query Match 9.8
Best Local Similarity 75.5
Matches 457; Conservative
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5'UTR
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/frequency= 0.12
/standard_name= "single nucleotide polymorphism"
/note= "marker 9-19-307 (All)"
delete(1535)
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/standard_name= "single nucleotide polymorphism"
/note= "marker 9-19-442 (A12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= ab
/frequency= 0.29
/standard_name= "single nucleotide polymorphism"
/notea = "marker 9-3-324 (Al5)"
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/frequency= 0.05
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/note= "marker 9-9-246 (A23)"
delete(20595..20597)
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/note= "marker 9-20-187 (Al3)"
replace(2391, G)
                                                                                                                                                                                                                                                                                                                                                                       /standard_name= "single nucleotide polymorphism"
/note= "marker 9-1-308 (A14)"
replace(3778,T)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /standard_name= "single nucleotide polymorphism"
/note= "marker 99-14419-424 (A16)"
replace(15007,A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /standard_name= "single nucleotide polymorphism"
/note= "marker 9-24-260 (A17)"
replace(15233,A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= ae
/frequency= 0.15
/standard_name= "single nucleotide polymorphism"
/note= "marker 9-24-486 (A18)"
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/standard_name="single nucleotide polymorphism"
/note="mark= 9-6-187 (A19)"
replace(19567,G)
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/frequency= 0.35
/standard_name= "single nucleotide polymorphism"
/note= "marker 9-7-148 (A20)"
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/note= "marker LSRX10-BM (A25)"
replace(606,T)
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/note= "marker A'l"
insert(5141,G)
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/standard_name= "single nucleotide polymorphism"
/note= "marker 9-7-325 (A21)"
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/standard_name= "single nucleotide polymorphism"
/note= "marker 9-7-367 (A22)"
replace(20158,G)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /frequency= 0.26
/note= "marker LSRX9-BM (17-1-240) (A24)"
replace(21108,G)
                                                                                                                                                                                          replace(1788, A)
                                                                                                                                                                                                                                                                                                                                                 /frequency= 0.24
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/*tag= ah
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/note= "marker 9-19-148 (A10)"
replace(1374,A)
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/note= "marker 17-2-297 (A31)"
/note= "potential 5' regulatory region"
2001..2356
/*tag= b
/number= 1
2357..3539
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/*tag= 9
//number= 3
15144..15200
/*tag= h
//number= 4
15201..15764
/*tag= i
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//wtag= n
//wmber= 7
//wtag= n
//wmber= 8
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//wtag= g
//wmber= 9
//wtag= g
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12163..12282
/*tag= f
/number= 3
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15765..15911
/*tag= j
10mber= 5
15912..19578
/*tag= k
/number= 5
/number= 5
/number= 6
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/number= 2
3885..12162
/*tag= e
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3540..3884
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Leptin; human; LSR; lipolysis stimulated receptor; obesity; hypertension; anorexia; cachexia; stroke; atherosclerosis; ds.
                                                                                                                                                                   Human leptin fragment coding sequence SEQ ID NO: 1.
                                                                                                                                                                                                                                                     regulatory region"
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complement(1244..1262)
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1..2000
/*tag= a
/note= "5' regulatory
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complement(819..837)
                                                                                                                                                                                                                                                                                                               complement(607..625)
                                                                                                                  AAF62331 standard; DNA; 23187 BP
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replace(1374,G)
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replace(1401,T)
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1096..1115
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1516..1534
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1382..1400
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946..963
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2966 aactcctgacctcaagtgatccacccacctgggcctcccaaagtgctgggattacaggca 3025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3060 aggictggagigcagiggigcgaicatagitcacigcagccicaaccicccaggcccaag 3119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /standard_name= "single nucleotide polymorphism"
        /standard_name= "single nucleotide polymorphism"
                                      /standard_name= "single nucleotide polymorphism"
/note= "marker A'3"
replace(8394,G)
                                                                                                                                         /standard_name= "single nucleotide polymorphism"
/note= "marker A 6"
delete(9950..9957)
/note= "marker A'7"
                                                                                                                                                                                                                                                                    /standard_name= "single nucleotide polymorphism"
/note= "marker A'10"
delete(19040)
                                                                                                                                                                                                                                                                                                      Length 23187;
                                                                       /standard_name= "single nucleotide polymorphism"
/note= "marker A'4"
                                                                                                  /*tag= aq
/standard_name= "single nucleotide polymorphism"
                                                                                                                                                                                                                                    /standard_name= "single nucleotide polymorphism"
                                                                                                                                                                                                                                                                                                                      36;
                                                                                                                                                                                                                                                                                                                      0; Mismatches 112; Indels
                                                                                                                                                                                                                                                                                                    Score 323.8; DB 21;
Pred. No. 2e-73;
                                                                                                                 /note= "marker A'5"
replace(9028,A)
                                                                                                                                                                                                                                           /note= "marker A'9"
replace(11878,T)
               /note= "marker A'2"
insert(7428,C)
                                                                                                                                                                                                           /note= "marker A'8"
                                                                                                                                                                                                                     replace(10021, A)
                                                                                                                                                                                   replace(9977,C)
                                                                                          replace(8704,C)
                                                                                                                                                                                                                                                                                                     Query Match 9.8%;
Best Local Similarity 75.5%;
Matches 457; Conservative (
                         variation
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Ouery Match
9.8%; Score 323.8; DB 22; Length 23187;
Best Local Similarity 75.5%; Pred. No. 2e-73;
Matches 457; Conservative 0; Mismatches 112; Indels 36; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= bx
10002..10020
/*tag= by
replace(10021,G)
/*tag= bz
complement(10022..10040)
                        /*tag bf /*tag bf /*tag bg /*tag bg 8375..7393 /*tag bh replace(8394,C) /*tag bi complement(8395..9413)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= ca
complement(10023..10040)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(10996..11015)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= cg
complement(11879..11897)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(12417..12436)
/*tag= cl
                                                                                                                                                                                                                                                                                                                                /*tag= bs
complement(9951..9969)
/*tag= bt
9958..9976
/*tag= bu
9964..9981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(10546..10563)
                                                                                                                                                                                                                                                                                                                                                                                                             replace(9977,T)
/*tag= bw
complement(9978..9996)
                                                                                                                     /*tag= bj
complement(8576..8593)
/*tag= bk
8685..8703
                                                                                                                                                                  /*tag= bl
replace(8704,T)
/*tag= bm
complement(8705..8723)
                                                                                                                                                                                                                                      /*tag= bo
replace(9028,G)
/*tag= bp
complement(9029..9047)
             complement(7429..7447)
/*tag= bf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  replace(11878,T)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= cb
10492..10512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= cd
11857..11877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= ch
11972..11990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= ci
12005..12023
                                                                                                                                                                                                                                                                                    /*tag= bg
9622..9639
/*tag= br
                                                                                                                                                                                                                                                                                                            /*tag= br
9931..9949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= ck
/number= 3
                                                                                                                                                                                                                  /*tag= bn
9009..9027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= cc
                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= bv
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              misc_binding
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                                                                                                        *tag= aa
2001..21190
**tag= ab
Product= "LSR"
**note= "this sequence contains introns"
2001..2356
                                                                                                                                                                                                                                                                                /*tag= ag
2372.2390
4.tag= ah
replace(2391,C)
/*tag= al
complement(2392.2410)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2036..2053

/*tag= ad

2062..2081

/*tag= ae

complement(2074..2093)

/*tag= af

2084..2102
            /*tag= w
complement(1616..1635)
                                                                                 /*tag= z
complement(1789..1807)
                                                                                                                                                                                                                                                                                                                                                        /*tag= aj
complement(2563..2580)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= ar
complement(3779..3797)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= bc
complement(7072..7089)
/*tag= bd
7409..7427
                                                                                                                                                                                                                                                                                                                                                                              /*tag= ak
complement(2470..2489)
                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= al
complement(2483..2500)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= as
complement(3882..3901)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tåg= at
complement(4336..4356)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= aw
complement(4902.4920)
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3759.3777
**tag= ap
3775.3792
/*tag= aq
replace(3778,T)
                                    /*tag= x
1769..1787
/*tag= y
replace(1788,C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4444..4463
/*tag= av
replace(4498,G)
                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= an
3540..3884
/*tag= ao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= ax
1979..4997
/*tag= ay
                                                                                                                                                                             /*tag= ac
/number= 1
                                                                                                                                                                                                                                                                                                                                                                                                                             1g= am
5..3474
 1602..1621
                                              misc_binding
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36; Gaps

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'note= "this sequence contains introns"
                                                                                                                                                                                                                                                                                       complement(10229..10247)
                                                                                                                                                                                                                                                                                                                                                         complement(10287..10305)
                                                                                                                                           complement(4602..4620)
                                                                                                                                                                                                                                                                /note= " binds probe"
replace(10228,T)
                                                                                                                      binds probe"
                                                                                                                                                                                                                                                                                                                                   binds probe"
                                                                                               /*tag= k
4589..4613
/*tag= 1
/note= " binds pr
replace(4601,G)
                 /*tag= g
/product= "PG-3"
                                                                                                                                                                                                                                                                                                                                           replace(10286,T)
                                                                                                                                                                                                                                                                                                                                                                   /*tag= z
replace(10370,)
/*tag= aa
10411..10430
/*tag= ab
26810..26897
                                                                                                                                                                                                                                                                                              /*tag= v
10267..10285
                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= ac
/label= "D"
31357..31471
/*tag= ad
/label= "E"
34261..34404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39877..39896
/*tag= ai
39925..39943
                                                                                                                                                                                       /*tag= p
10007..10025
/*tag= q
10115..10233
                                                                                                                                                                                                                     /*tag= r
/label= "C"
10209..10227
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= ae
/label= "F"
37377..37466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= af
/label= "S"
39704.40858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= ag
/label= "T"
39556..39574
/*tag= ah
39877..39896
                                                                                                                                                                                                                                                                                                             /*tag= w
10274..10298
                                                                                                                                                                                                                                           /*tag= s
10216..10240
                                                                                                                                                                 /*tag= o
/label= "B"
4891..4908
/*tag= p
10007..10025
                                                  /label= "A"
2108..2125
/*tag= i
4559..4577
/*tag= j
4582..4600
                                                                                                                                                    /*tag= n
4627..4718
                                    ..2079
                                                                                                                                     /*tag= m
                                                                                                                                                                                                                                                                                                                            /*tag= x
                                                                                                                                                                                                                                                          /*tag= t
/note= " ]
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                                      exon
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        CDS
 3119
                                            6462
                                                          2905
                                                                         6402
                                                                                        2962
                                                                                                      6342
                                                                                                                     6162
                                                                                                                                                                                                                                                          6042
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2726 caagacetttetettttttgttatttttttgtgttttttg33ctttgagacagagtettgatetgttgc 2785
                                                                                                                                                   tgagccaccgtgcctggcctgttt-----tttgaaatg 3059
                                                                                                                                                           3120 tgatcctcctgcctcagccccttgagtagctggggctacaggcgcacaccaccatgcctg 3179
                                                                                                                                                                                                                      gct-----agtttttaaaaatttttgtggagatgaggtttcactatgttgtccaggct 3231
                                                                                                                                                                                                                                                                         3232 aatcttgaactcctcggcttaagcaaccctctggtctcagcctcccacagtgctaggatt 3291
                                                          3060 aggictggagigcagiggiggigcgaicatagitcacigcagccicaaccicccaggcccaag
                                                                                                                                                                                        ggctaatttttgtatttttagtagagacagggtttcaccatgttggccagactggtctca
        ccaggccagagtgcagtggcacgatctcagctcactgcaacctccgccttccaggttcaa
                                      Human; PG-3; cancer; BRCA1; chromosome 8p23; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         regulatory region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= e
complement(2000..2018)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= d
/note= " binds probe"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
1..2000
                                                                                                                                                                                                                                                                                                                                                          AAF24497 standard; cDNA; 240825 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     replace(1999,C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1823..1840
/*tag= b
1980..1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= a
/note= "5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..2011
                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1987
                                                                                                                                                                                                                                                                                                                                                                                                      Human PG-3 gene.
                                                                                                                                                                                                                                                                                                      3292 acaag 3296
                                                                                                                                                                                                                                                                                                                     5981 TACAG 5977
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/*tag= bg
complement(42233..42251)
/*tag= bh
42526..42543
/*tag= bi
/*tag= bi
                                                                                                                                                                                                                                                                           Complement(41405..41423)

**tag= bb

41564..41581

**tag= bc
42122..42141

**tag= bd
42213..42231

**tag= be
42220..42244
                                                                                                                                                                                                                            omplement(41386..41404)
                                          complement(39945..39963)
                                                                                                                       complement(39974..39992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(67476..67494)
/*tag= aj
39932..39956
/*tag= ak
/note= " binds probe"
                                                                                                                                                                                                                                                                                                                                         /*tag bf
/note " binds probe"
replace(42232,C)
                                                                                                                                                                                                                                          41392.41416
/*tag= az
/note=" binds probe"
replace(41404,C)
                                                                                           *tag= ap
note= " binds probe"
eplace(39973,C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probe,
                                                                                                                                                                                    /*tag= av
/note= " binds pr
replace(41385,C)
/*tag= aw
/1385..41403
                            eplace(39944,T)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note= " binds preplace(67475,G)
                                                                /*tag= an
39954..39972
/*tag= ao
39961..39985
                                                                                                                             /*tag= ar
40242..40259
/*tag= as
41137..41154
/*tag= at
41366..41384
                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= bj
/label= "G"
57289..67309
/*tag= bk
                                                                                                                                                                                                                                                                                                                                                                                                                                    67456..67474
/*tag= bl
67463..67487
/*tag= bm
/note= "bind:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= bo
67724..67741
/*tag= bp
69182..69200
                                                  '*tag= am
9953..39970
                                                                                                                                                                       *tag= au
1373..71397
                                                                                                                *tag= ag
                                    *tag= al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               *tag=
       misc_binding
                                                                                   misc_binding
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The present invention describes an isolated, putilied or recombination of polynucleotide (PN) (I) comprising a configuous span of 8 to 50 nucleotides, where the span includes a G713 or chromosome 13431-433 as a G713 gene expression inhibitor. (I) can be used genotyping to estimate the frequency of an allele of a G713 or chromosome 13431-433 celated biallelic marker in a population, and of a haplotype for a set of biallelic marker in a population, and of a haplotype for a set of biallelic markers in a population, and of a haplotype for a set of biallelic markers in a population, and of a haplotype for a set of biallelic markers in a population, and of a haplotype for a set of detecting an association between a genotype and a trait. The frequency is used for detecting an association between a genotype and a trait being schizophrenia. The genotype is used to determine whether an individual is at risk of developing schizophrenia. (I) can also be used as a medicament against several disorders preferably brain, psychiatric disorders such as schizophrenia and bipolar disorder. Early identification of risk of developing schizophrenia is possible, which would enable early and/or prophylactic treatment. AAA55964 to AAA55966 represent human G713 genomic DNA sequences; AAA55967 encodes the human C713 genomic DNA sequences; AAA55967, and AAA56031 and AAA56032 represent PCR primers used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present invention describes an isolated, purified or recombinant
                                                                                                                                                                                     Human; chromosome 13; G713; chromosome 13q31-q33; schizophrenia; blallelic marker; polymorphism; central nervous disease; detection; neuroleptic; G713 gene expression inhibitor; genotyping; brain disorder; psychiatric disorder; bipolar disorder; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel polynucleotide of human G713 gene useful for diagnosis and prophylactic treatment of brain, psychiatric disorders like schizophrenia and bipolar disorders
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                 AAA55965 standard; DNA; 21278 BP
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9.7%; Score 320.6; DB 21; Length 21278; 76.3%; Pred. No. 1.3e-72; Live 0; Mismatches 129; Indels 6;

Best Local Similarity 76.3 Matches 434; Conservative

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Query Match

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SmaI; A min1-library was made by cloning products derived
from ONESTES POR (U.S. Letters Patent application No. 196
.716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010,
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                                                                                                             /db_xref="taxon; oser.co."/db_xref="taxon; o
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1 (bases 1 to 371)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-JUN-2001
CDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    aggocagagtgcagtggcacgattcagctcactgcaactccgccttccaggttcaact 2847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3027
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gctggggctacaggcgcacaccaccaccgctggctagtttttaaaattttgtggagatg 3207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115 GCTGGGGCTACAGGCGCACACCATGCCTGGCTAGTTTTTAAAATTTTTGTGAAAATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 446.6; DB 11; Length
Pred. No. 1.4e-43;
0; Mismatches 9; Indels
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                                                                                             /organism="Homo sapiens"
                         sequence stop: 363.
                                                                                                                                                                                                                                                                                                                                       stringency conditions.
     sequence start: 31
                                                  Location/Qualifiers
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98.0%;
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High quality
High quality
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Best Local S
Matches 452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KEYWORDS
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 344)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="CIT Approved Human Genomic Sperm Library D"
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DEFINITION HS_5505_A1_C09_T7A RPCI-11 Human Male BAC Library Homo sapiens
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sapiens genomic clone Plate=2253 Col=19 Row=N, DNA sequence.
AQ069145
                                                                                                                                                                                                                       Sequence-tagged connectors: A sequence approach to mapping scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ATCTCAGCTCACTGCAACCTCCGCCTTCCAGGTTCAACTGGTTCTCCTGCCTCAGCCTCC
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                                                                                                                                                                                                                                                                                                                                       High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3818
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 338.8; DB 13; Length
Pred. No. 6.7e-31;
0; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=2253 Col=19 Row=N"
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                                                                                                                                                                                                                                                                                                                       Contact: Mahairas GG, Wallace JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 344.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence Tagged Connector
Plate: 2253 row: N column: 19
Class: BAC ends
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98.8%;
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                                                                                                     Homo sapiens
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                           ACCESSION
                                                                                                                                                             REFERENCE
                                                                                                                                                                                   AUTHORS
                                               VERSION
KEYWORDS
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High Throughput Sequencing Center University of Mashington 401 Queen Anne Avenue North, Seattle, WA 98109, USA 101 Queen Anne Avenue North, Seattle, WA 98109, USA 7e1: (206) 616-3868
Fax: (206) 616-3868
Fax: (206) 616-3888
Email: jwallacedu.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu,ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu
Plate: 1081 row: E column: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pBACe3.6; Site_1: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ϊ;
                                                                                                                                           Euteleostomi;
                                                                                                                                                                                                       Mahairas, G.G., Waliace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            598 GGAGTACAGTGGTGCAATCTCAGCTCACTGCAACCTTCGCCTCCCAGGTTCAAGCAATTC 539
                                                                                                                                                                                                                                                                              Sequence-tagged connectors: A sequence approach to mapping
                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="RPCI-11 Human Male BAC Library" /sex="male"
clone Plate=1081 Col=17 Row=E, DNA sequence
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/db_xref="taxon:9606"
/clone="Plate=1081 Col=17 Row=E"
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Location/Qualifiers
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Poustka,A., Wellenreuther,R., Mewes,H.W., Weil,B. and Wiemann,S.).
EST (Poustka,A., Wellenreuther,R., Mewes,H.W., Weil,B. and Wiemann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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6, 14059
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: poustkamping-berlin-dahlem.mpg.de
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2): Fmail S. Wiemann@dkfz- heidelberg.de;
sequenced by DKF2 (German Cancer Research Center,
Heidelberg/Germanny) within the CDNA sequencing consortium of the
---tgaaatgag 3061
                                                                                                                                                                                           tagtttttaaaaatttttgtggagatgaggtttcactatgttgtccaggctaatcttgaac 3241
                                                                                                                            3122 atcctcctgcctcagccccttgagtagctggggctacaggcgcacaccaccatgcctggc 3181
                                                                                                                                              CCGCACCCAACCAGTAATTTTTTTTTTTTTTTGAGATGGAGTCTCACTCTGTTACCCA 299
                                                                                                                                                                                                                                                                                                                                                                  AL597806 642 bp mRNA EST 14-AUG-2001
DKFZp31300116_r1 313 (synonym: hlcc2) Homo sapiens cDNA clone
DKFZp31300116_5', mRNA sequence.
AL597806.1 GI:15160497
                                                           3062 gtctggagtgcagtggggtgcgatcatagttcactgcagctccaactcccaggcccaagtg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              No sl sequence available.
This clone (DKF2p31300116) is available at the RZPD in Please contact the RZPD: Ressourcenzentrum, Heubnerweg Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 642;
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Pred. No. 7.3e-29;
0; Mismatches 120; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Poustka A.J.
Department Lehrach
Max-Planck-Institute for Molecular Genetics
Ihnestrasse 73, 14195 Berlin, Germany
Far: +49-30-84131128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="DKFZp31300116"
/clone_lib="313" (synonym: hlcc2)"
/dev_stage="adult"
/lab_host="DH108"
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/db_xref="taxon:9606"
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TITLE
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Gaps

25;

Conservative

Matches 447;

Similarity

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Uppublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.a column: 08
Plate: LLAMA423 row: a column: 08
High quality sequence stop: 661.
Location/Qualifiers
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600 TTATTTTTAATTTTATTTTTAATTTTTTGAGACCGAGTCTCACTCTGTCACCCAGGCT
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/db_xref="taxon:9606"
/clone="IMAGE:4153999"
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BF346320
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1 (bases 1 to 595)

1 (base 1 to 595)

2 (base 1 to 595)

3 (base 1 to 595)
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MR2-CI0128-051200-003-f10 CI0128 Homo sapiens cDNA, mRNA sequence.
BF816106
BF816106.1 GI:12151177
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Oligo dT.
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            /tissue_type="anaplastic oligodendroglioma with 1p/19q
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                                                                                                                                                                                                     Gaps
                                                    /note="Organ: brain; Vector: pCMV-SPORT6; Site_1:
Site_2: Sal1; Cloned unidirectionally. Primer: Oli
Average insert size 2.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
161 c 191 g 127 t
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                       Length 679;
                                                                                                                                                                     Score 317.4; DB 11; Length
Pred. No. 1.4e-28;
0; Mismatches 111; Indels
                                       /lab_host="DH10B (Tl phage-resistant)"
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/clone_lib="NCI_CGAP_Brn67"
                                                                                                                                                                       9.68;
76.18;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="cl0128"
/dev_stage="Adult"
/note="Organ: colon_ins; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
Site_2: SmaI; A mini-library was made by cloning products
Gerived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions.
11 a 162 c 154 g 167 t lothers
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Seq primer: puc IB forward
High quality sequence stop: 468.
                                                                                                                                                                                                Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                 expressed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpsondiudwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer
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Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J.
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                            Simpson, A.J. Shotgun sequencing of the human transcriptome with ORF
                                                                                                97 (7), 3491-3496 (2000)
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Pred. No. 2.4e-28;
0; Mismatches 113; Indels
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                                                                                                                                                 Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
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ilarity 75.7%;
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Ansorge, W., Wirkner, U., Mewes, W., Weil, B. and Wiemann, S. EST (Ansorge, W., Wirkner, U., Mewes, H.W., Weil, B. and Wiemann, S.) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                  Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKE2): Email s.wiemann@dkfz- heidelberg.de;
sequenced by EMBL (European Molecular Biology Laboratories,
Heidelberg/Germany) within the CDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               German Genome Project.

No sl sequence available.

This clone (DKPZp547E2I7) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
3206 tgaggtttcactatgttgtccaggctaatcttgaactcctcggcttaagcaaccctctgg 3265
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DKFZp547E217_r1 547 (synonym: hfbr1) Homo sapiens cDNA clone
DKFZp547E217 5', mRNA sequence.
                Site_1: NotI; Site_2: SalI"
168 t l others
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Pred. No. 1.2e-27;
0; Mismatches 113; Indels
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/organism="Homo sapiens"
/organism="taxon:9606"
/clone="bkFzp547E217"
/clone_lib="547 (synonym: hfbr1)"
/tissue_type="brain"
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166 c 156 q
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                                                               tctcagcctcccacagtgctagga 3289
                                                                               /dev_stage="fetal
                                                                                                                                                                                                                                         AL138254.1 GI:6854935
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Molecular cloning of the chromosomal breakpoint in the LIS1 gene of a patient with isolated lissencephaly and balanced t(8:17) Hum. Genet. (1998) In press Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (09-MRR-1998) to the DDBJ/EMBL/GenBank databases. Hiroki Kurahashi, Biomedical Research Center, Osaka University Medical School, Division of Clinical Genetics, Department of Medical Genetics, 2-2 Yamadaoka, Suita, Osaka 565-0871, Japan (E-mail:kura@cigene.med.osaka-u.ac.jp, Tel:81-6-879-3381, Pax:81-6-879-3389)
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                                                                 atcccaccactgcacttaagcctggataacaaagcaagaccctgtctcaaataacaatag 1476
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                                                                                                    307 GATGGCTTGAGCCCAGGAGTTTGAGACCAGCCTGGGCAACATGGTGAAACCCTGTCCCTG
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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74.2%; Pred. No. 6.8e-28;
1ve 0; Mismatches 120;
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Kurahashi,H.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

( bases 1 to 603)

Ansorge,W., Wirkner,U., Mewes,W., Weil,B. and Wiemann,S.

Err (Ansorge,W., Wirkner,U., Mewes,H.W., Well,B. and Wiemann,S.)

Contact: Ansorge W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Am Klopferspitz 18a D-82152 Martinsried, Germany This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de; sequenced by EMBL (Buropean Molecular Biology Laboratories, Heidelberg/Germany) within the cDNA sequencing consortium of the German Genome Project.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      No s1 sequence available.
This clone (DKF2p547E217) is available at the R2PD in Berlin.
Please contact the R2PD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERWANY: Email: clone@rzpd.de.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                  3184 gittitaaaailitigiggagaigaggittcaclaigtigiccaggctaaictigaacic 3243
                                                                                                            gaceteaagtgatecaceceacetgggeeteceaaagtgetggggattacaggeatgageca 3032
                                                                                                                                                                          2876 CAGGAGTGCAATGGCGTGATCTTGGCTCACTGCAACCTCCACCTCCCAGGTTCAAGAGAT 2935
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2638 TTCTGCCTCAGCCTCCTGAGTAGCTGGGATTACAGGCATGCGCAACCACGCGGGGTAAT
                                                                                                                           2758 GACCCC--GTGATCCTCCCCACCTTGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCA
                                                                                                                                                                                           ctggagtgcagtggtgcgatcatagttcactgcagcctcaacctcccaggcccaagtgat
                                                            2698 TTTTGTATTTTTAGTAGGATGGGGTTTCACCATGTTGGTCAGACTGGTCAAACTCCT
                                              ttttgtatttttagtagagacagggtttcaccatgttggccagactggtctcaaactcct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pAMP1; Site_1: Not1; Site_2: Sal1"
166 c 156 g 168 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="DKFZp547217"
/clone_lib="547 (synonym: hfbrl)"
/tissue_type="brain"
/dev_stage="fetal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
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S NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Uppublished (1999)
C contact: Robert Strausberg, Ph.D.
Email: cgapbs-femail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Prayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL)
thtp://image.llnl.gov
Plate: LLCM1521 row: i column: 13
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ctgcagcctcaacctcccaggcccaagtgatcctcctgcctcagcccttgagtagctgg 3152
                                                                                                      2734 ttetetttittgitalttittitgigettitgagacagagiettigatettgitgeecaggeea 2793
                                                                                                                                                                                                             2794 gagtgcagtggcacgatctcagctcactgcaacctccgccttccaggttcaactggttct 2853
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                                                                                                                                                                                                                                      55 TTTGTTTTGCTTTGGTTTGGTTTTNAGACGGGTCTCGCTCTCGCTCACCCAGGCTG 114
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602571053F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4695636
                                                                                                                                                                                                                                                                                                                                                     175 CCCGCCTCAGCCTCCAAAGTAGCCGGGACTACAGGTGTGCGCCACCACGCCGGCCAATT
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  Length
  DB 10;
                                               0; Mismatches 145;
Score 305.6; DB ]
Pred. No. 3.6e-27;
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9.38;
                                                    Conservative
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BG542878
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Query Match
Best Local Similarity
Matches 403; Conserv
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                                                                                                                                         /clone_lib="NIH_MGC_77"
/lab_host="DH10B (Tl phage-resistant)"
/lab_host="DH10B (Tl phage-resist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7
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602625376F1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4750146 5′,
BG677697
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               174 TGGGACTACAGGCAGATGCCACCACGCCCAGTTAGTTTTTGTATCTTTGGTAGAGACAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 753;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.3%; Score 305.4; DB 11; Length 74.2%; Pred. No. 3.4e-27; tive 0; Mismatches 126; Indels
                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
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sequence stop: 693
                                                                                                                         /clone="IMAGE:4695636"
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ACCESSION

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/tissue_type="squamous cell carcinoma" / Tlab_most="DH10B (Tl phage-realstant)." / Tlab_most="DH10B (Tl phage-realstant)." / Anote="Organ: skin; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.5kb. Library constructed by Life Technologies. Note: this is a NCI_CGAP Library." by Life 180 c 230 g 258 t
                                                                                                        Euteleostomi;
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                                                                                                                                            1 (bases 1 to 963)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                Email: CapDS-remail.nth.gov
Tissue Procurement: James Cleaver, M.D.
CDNA Library Preparation: Life Technolaies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can bttp://image.llnl.gov
http://image.llnl.gov
High quality sequence stop: 780.
High quality sequence stop: 780.
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                                                                                                  Chordata; Craniata; Vertebrata; E
Primates; Catarrhini; Hominidae;
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llarity 73.9%; Pred. No. 3.8e-27;
Conservative 0; Mismatches 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:4750146"
/clone_lib="NCI_CGAP_Skn4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
GI:13909107
                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                            Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-remail.nh.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLCM1071 row: k column: 15
High quality sequence stop: 562.
1. 7702
                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 702)
NIH-MGC http://mgc.noi.nih.gov/.
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                                                                                                                                                 BF678427 702 bp. mRNA EST 21-DEC-2000 602085862F1 NIH_MGC_83 Homo sapiens CDNA clone IMAGE:4250246 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         525 GGAGTGCTATGGCGGAATCTCGGCTCACTGCAGCCTCCGCTTCAAATGATTC
                         587 -GTTTTAGTAGAGGTGGGGATTTTGCCATGTCACCCAGGCTGGTCTCGAACTCCTGAGCT
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                                                  0; Mismatches 121; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4250246"
                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="NIH_MGC_83"
/lab_host="DH10B (T1 ph
                                                                                                                                                                                                      BF678427.1 GI:11952322
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                                                                                                                                                                              mRNA sequence.
BF678427
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                                                                                                                                     BF678427/c
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Homo sapiens
Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Mamanla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Mamalia: Lo 856)
Mahairas, G.C., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AQ891549 856 bp DNA GSS 10-NOV-1999 HS_3143_A1_C12_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3143 Col=23 Row=E, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High Throughput Sequencing Center University of Washington University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618 Fax: (206) 616-3887 Enail: jwallace@u.washington.edu Enail: jwallace@u.washington.edu BAC end Web Server: http://www.htsc.washington.edu BAC end Web Server: http://www.htsc.washington.edu Plate: 3143 row: E column: 23 Seq primer: T?
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                                                                                                                                                                                                                                                                                                                                             atcatagttcactgcagcttcaacctcccaggcccaagtgatcctcctgcctcagccct 3141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gcagtggtgcg 3081
                                                                                                                                                                                                                                                                                                                                                                                                                                                            3142 tgagtagetggggctacaggcgcacaccatgcctggctagttttaaaatttttgtg 3201
2913 ttttgtatttttagtagagacagggtttcaccatgttggccagactggtctcaaactcct 2972
                                                                                                                                                                                                                                                            167 CCAGTAGCTAGGACTACATGCGTGCATCTCCACGCCTGGCTAATTTTTGTGTTTTTTGTTA 108
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                                                                                                                                                                                                                                                                                                                                                                                                      227 ATCTCGGCTCACTGCAACCTCTGCCTCTTGGATTCAAGCGATTCTCCTGCCTCAGCCTTT 168
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/db_xref="taxon:9606"
/clone="plate=3143 Col=23 Row=E"
/clone_lib="CIT Approved Human Genomic Sperm Library
/sex="male"
                              405 TTTTGTATTTTTAGTAGAGACAGGGTTTCACCATGTTGACCAGGCTGGCCTCGAACTCCT
                                                                                                                  gacctcaagtgatccacccacctgggcctcccaaagtgctgggattacaggcatgagcca
                                                                                                                                          Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
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                                                                                                                                                                                                                              ccgtgcctggcttttttgaaatgaggtctggagt-
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Location/Qualifiers
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AQ891549.1 GI:6347739
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 660)
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Unpublished (1997)
Other_GSSs: RPCIII-135N16.TJ
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Other_SSs: RPCIII-135N16.TJ
Other_SSs: RPCIII-0, William Nierman, Maj
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 2085
Fax: 301 838 0200
Score 303.4; DB
Pred. No. 5.4e-27
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Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html Seq primer: T7
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RPCIII Human Male BAC Library"
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/db_xref="texon:9606"
/clone="RPCT-11-135N16"
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/sex="Male"
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SUMMARIES

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4444 Forest Park Parkway, St. Louis,
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4444 Forest Park Parkway, St. Louis,
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4444 Forest Park Parkway, St. Louis,
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Submitted (12-MAY-2000) Genome Se
University School of Medicine, 44
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5 (bases 1 to 124526)
Waterston, R. H.
                                                           Submitted (12-JUN-1998) Genome University School of Medicine, MO 63108, USA
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3 (bases 1 to 124526)
Waterston, R.H.
Direct Submission
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

Web site: http://genome.wustl.edu/gsc Contact: sapiens@watson.wustl.edu

code: WUGSC

Center

Center project name: H_RG269P13

all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by This sequence was finished as follows unless otherwise noted: restriction digest.

MAPPING INFORMATION:

The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/plk/GTB/CHR7, send mailto:egreen@hgri.nih.gov/ or see http://genome.wustl.edu/gsc

SOURCE INFORMATION:

Clone CTA-269P13 is from a release of the human BAC library CTB-HS-A. The library contains cloned DNA from human sperm. See Shizuya et al., Proc. Natl. Acad. Sci. USA 89:8794-7 (1992); U-J. Kim et al., Genomics 34:213-8 (1996). The clone is available from Research Genetics, Inc. (http://www.resgen.com) VECTOR: pBeloBAC11

chloramphenicol Selection:

The clone sequenced to the left is RP4-754G14; the clone sequenced to the right is RP11-396K3. Actual start of this clone is at base position 1 of CTA-269P13; actual end is at base position 124526 of CTA-269P13. NEIGHBORING SEQUENCE INFORMATION:

The clone CTA-269P13 may contain a transposon in the growth of the clone, which is not part of the submitted sequence.

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	1801 cgacgggaaggacaagtgtaaaccetttccttgtccctgcaggtgtgtgtgtgaacatgag 1860	1921 agccettetgtaccetecetgececetgtecegacagacagacatectett 1980	2041 ggggacaccttcatccgtcacatcgcctgctgggctttgggaagcgcttcgtacccagc 2100 08003 GGGACACCTTCATCCGTCACATCGCCTGTGGGCTTTGAGAAGCGCTTTCGTACCCAGC 108062 2101 cagcactatgtgagtagctggtggagggcatcccgtgggggaatacgggaggacagca 2160 101 cagcactatgtgagtagctggtggagggcatcccgtggggggaatacgggaggga	cagggtet 2	uggectorgreecount to the control of	2341 gccctcagccttagccaggagtcctcttctgctccctgccatggccaggcagccagc	108363 GCTCTCTCAGGTCCGAGGCCCACTCCTCAGGAAGCCTTCCCTGACTAGCCTATCA	ctccagtagg 	2581 gagtcctcccatctgtccccaaggaggctggacaaatgcctgctcagacacacaagtcca 2640 [11] [11] [11] [11] [11] [11] [11] [11]
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Opportished

S (Dases 1 to 169604)

S Waterston, R. H.

Direct Submission

University School of Medicine, 4444 Forest Parkway, St. Louis,

MO 63108, USA

B (Dases 1 to 169604)

Materston, R. H.

Direct Submission

L Submitted (23-WAY-2001) Genome Sequencing Center, Washington

University School of Medicine, 4444 Forest Park Parkway, St. Louis,

MO 63108, USA

On May 23, 2001 this sequence version replaced gi:13431264.

Location/Qualifiers
                               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 169604)
Waterston, R. H.
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Homo sapiens clone RP11-813J7, complete sequence.
AC083884
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Sequencing Center, Washington
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On Jul 15, 2000 this sequence version replaced
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Threide, J., Abbott, A., Graves, T.
The sequence of Homo sapiens BAC
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University School of Medicine,
MO 63108, USA
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restriction digest.

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5254. .5330
/note="similar to EST AA794004 (NID:92856959) vr37a02.rl"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST AA794004 (NID:92856959) vr37a02.rl"
                   EST AI700706 (NID:94988606) we39e12.x1"
                                                                                                                                   EST A1696334 (NID:94984234) tw59e05.x1"
                                                                                                                                                                                                                                                                                                                                EST AI700706 (NID:94988606) we39e12.x1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST AW163398 (NID:g6302431) au94g04.yl"
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                                                                                               EST T79157 (NID:g697666) yd70b07.s1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3267.6; DB 9; Length 230552;
No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                         EST AW523936 (NID:97166321)"
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                                                                                                                                                                                                                                                                                          AW503416 (NID:97139965)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                               EST T31784 (NID:g613882)"
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                                                           EST T31784 (NID:g613882)"
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                                                                                                                                                                                              /rpt_family="Mariner"
5254. .5330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6637. .6883
/note="similar to 6884. .7119
/note="similar to E6906. .7117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7514. .7697
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/note="similar to F7514. .7689
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                                                                                                                                                                                                                                                                                              5265. .5330
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5964. 6127
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6032. 6370
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7426_.7476
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7510..7697
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7514..7697
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/note="similar to
5265. .5348
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5305. .5330
/note="similar to
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/note="similar to
5265. .5330
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3871. .3932
/note="similar to
                                                           /note="similar to 3889. .4387
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/note="similar to
                                                                                                                 4109. .4387
/note="similar to
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/note="similar to
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/note="similar to
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                                                                                                                                                       4502. .4812
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/rpt_family="Alu"
6637. .6883
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="similar
7514. .7695
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99.8%;
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7514. .7
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                               The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7, send mailto:egreen@nhgri.nih.gov , or see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence CTA-350L10 from base position 222330 to 222775 is a GA rich region. The sequence is not exact but it is believed to be the best representation of this region. The region was sized by PCR from clone DNA at 650 bp. The region corresponds to restriction digest hindili: band size 7685 in silico and 7756 real.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST AI566941 (NID:g4525393) tn25b07.x1"
                                                                                                                                                                                                                            Clone CTA-350L10 is from a release of the human BAC library CTB-HS-A. The library contains cloned DNA from human sperm. See: Shizuya et al., Proc. Natl. Acad. Sci. USA 89:8794-7 (1992); U-J. Kim et al., Genomics 34:213-8 (1996). The clone is available from Research Genetics, Inc. (http://www.resgen.com).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST AW197058 (NID:g6476288) xb15f09.x1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST H89808 (NID:91080238) yu82g03.rl"
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                                                                                                                                                                                                                                                                                                                                                                                                       Actual start of this clone is at base position 1 of CTA-350L10; actual end is at base position 230552 of CTA-350L10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST BE000775 (NID:98261008)"
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    .230552
    /organism="Homo sapiens"
/db_xref="taxon:9606"

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/clone_lib="CITB-HS-A"
441. .725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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3599. .4017
/note="similar to
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3240...3391
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/note="similar to
2337. .2682
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/note="similar to
1609. .1864
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/note="similar to
3820. .3932
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/note="similar to
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.054. .3367
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/map="7q11.2"
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sd	60 47095	120 47155	180 47215	240 47275	300 47335	360 47395	420 47455	480 47515	540 47575	600 47635	660 47695	720	780 47815	840 47875	900 47935	960	1020	1080 48113
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Σ	Qy Dp	QY Db	Qy Db	Qy Db	Qy	Oy Dp	Qy Db	Qy Db	Qy Db	QY Dp	QY	Qy Db	Qy Db	QY	Qy	Qy Db	Qy Db	Oy Db

aggt 1140 AGGT 48173	ccat 1200	CA :		taac 132	inac 4033 atem 1380	ATCG 484	cct	CCTG 48	taaa 1500	000	gctg 1360 GCTG 48592	gagg 162	 GAGG 48652	gaac 1680	GAA	aatg 17	AAT	cagg 1800	CAG	tgag 1860	TGA	gcaa 1920	GCA	cttt 1980	CTT	catg 2040	CAT	cagc 2100	CAGC	0316
aatoccagotactoaggagactaaogcaagagaattgottgaaocoaggaggcag; 	geggtgagecgagategegecattgeaetecagectgggaacaagagegagaete	JGGTGAGCCCAGATCGCGCCATTGCACTCCTGGGAAACAACAAGAGCGAGACT SAAAAAAAAAAAAATTGGGGCCATTGCAGGTGAGGAAGAAAAAAAA		accatcctgggcaacatagcaggaccctgtctgtacaaaaaaattaaaaaaatt. 	CCTICCIGGCCCAACAIRGCAGGACCCIGICIGIACAAAAAAAAIIAAAAAIII GGCAFGGTGGGGGGGGGGGGAGTGGGGAGTAGTGCGAGAGGCTGAGGAGGGGGGGG		ggagoccaggagttggaggctgcagtgaactgtgatccaccaccacctgcacttaag	GCTGCAGTGAACTGTGATCCCACCACTGCACTTAAG	aagcaagacctgtctcaataacatagcatagaataataataaaagaaat 		ycaa.c.cycyg.cyg.cyg.cyg.cyg.cyg.cyg.cyc.gyc.g	aaaggtatgaggtttgctatgcaatgtgaagttatcaaggaagg		gacatttgagcagagaaatggaggagagttatggagggaagatggtgaatggggg	ACATTTGAGCAGAGAAATGGAGGAGAGGTTATGGAGGGAAGATGGTGATGTGT	tggtcaagaccaggaatatggtcaaggggggaaagatggtcaaggggacgcagca.	sgrcaagaccaggaaratggrcaaggggggaaagarggrcaaggggacgagga	aaaggcctgaggcaggagcagcttgattcacccccaaaacccgtggggcccgtg	Secericascascascascaricationscoccanances	gacgggaaggacaagtgtaaacccttttccttgtccctgcaggtgtgtgt	acgggaaggacaagigtaaacctititctitgtcctgcaggaggigigigaaca	ctgcccatgtttacaccctgcaagcctgaagagtccccagaaactgaagaagaaa	TGCCCATGTTTACACCCTGCAAGCCTGAAGAGTCCCCAGAAACTGAAAGAAGAA	gcctttctgtaccctcctgcccctgtccgaccgcgacaaaagcgactcct.	CCCTTTCTGTACCCTCCCTGCCCCTGTCCCGACGCGACAAAAGCGACTTCCT	cagtgcatttaaggcgcagcctggaagtgccagggagcactggaggccaccagt	STGCATITAAGGCGCAGCCTGGAAGTGCCAGGGAGCACTGGAGGCCACCCAG	gggacacetteatecgteacategeeetgetgggetttgagaagegettegtace	GGACACCTTCATCCGTCACATCGCCCTGCTGGGCTTTGAGAAGCGCTTCGTAC	
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Missouri 63108, USA
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                                                                                                                                                                                                                                                                                                                                   Euteleostomi;
Washington
Missouri 63108,
                                                                                                                                         AC004883 131359 bp DNA PRI 21-DEC-1999
Homo sapiens PAC clone RP4-771P4 from 7q11.21-q11.23, complete
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Submitted (21-DEC-1999) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 6:
On Feb 24, 1999 this sequence version replaced gi:3309099.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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4444 Forest Park Parkway,
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Kalicki,J. and LaPlant,Y.
The sequence of Homo sapiens PAC clone RP4-771P4
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Submitted (20-FEB-1999) Department of Genetics,
University, 4444 Forest Park Avenue, St. Louis,
5 (bases 1 to 131359)
Waterston, R.
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Submitted (18-MRR-1999) Department of Genetics,
University, 4444 Forest Park Avenue, St. Louis,
6 (bases 1 to 131359)
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Contact: sapiens@watson.wustl.edu
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Genome Res. 8 (11), 1097-1108 (1998)
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Submitted (12-JUN-1998) Genome Se
University School of Medicine, 44
MO 63108, USA
4 (bases 1 to 131359)
Waterston, R.
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Sulston, J.E. and Water:
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                                                                                                                                                                                                                                                                                                             Homo sapiens
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Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu) using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994). The library is from
Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgil.nih.gov/DIR/CHR7, send mailto:egreen@nhgil.nih.gov, or see http://genome.wustl.edu/gsc
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note="similar to EST AI346557 (NID:94083763) qp46d02.x1"
                                                                                                                                                              This clone was derived from human PAC library RPCI-4, prepared by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127. 7471
'note="match to EST AI149529 (NID:93677998) qc70f05.x1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA525914 (NID:g2267983) ni6le09.s1"
                                                                                                                                                                                                                                                                                                                                                                               The clone sequenced to the left is RPS-1186P10. Actual start of this clone is at base position 1 of RP4-771P4; actual end is at 131359 of RP4-771P4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /rpt_family="Alu"
3424    .3947
/note="match to EST N39030 (NID:g1162237) yv22d08.s1"
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'note="match to EST H66847 (NID:g1025587) yr71c03.s1"
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'note="match to EST H68467 (NID:91027207) yr83h06.rl"
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                                                                                                                                                                                                                                               one male donor.

The clone may be obtained either from Genome Systems, Inc. (http://www.genomesystems.com) or Research Genetics, Inc. (http://www.resgen.com); or from Pieter de Jong.

VECTOR: pCYPAC2
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/note="match to EST N48220
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6359. .6671
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/db_xref="taxon:9606"
/chromosome="7"
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/clone="RP4-771P4"
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'note="match to EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
1. .131359
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5005. .5265
/rpt_family="Alu"
5268. .5501
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697. .7001
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7884. .7937
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VPEPANAGKRKVREFNFEKWNARITDLRKQVEELFERKYAQAIKAKGPVTIPYPLFQS
HVEDLYVEGLPEGIPFRRPSTYGIPRLERILLAKERIRFVIKKHELLNSTREDLOLDK
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KVKTEPTEDSGISLEMAAVTVKEESEDPDYYQYNIQAGPSETDDVDEKQPLSKPLQGS
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ERLSKVEKARQLREQVNDLFSRKFGEAIGMGFPVKVPYRKITINPGCVVVDGMPPGVS
FKAPSYLEISSMRRILDSAEFIKFTVIRPFPGLVINNQLVDQSESEGPVIQESAEPSQ
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ENIPFRSPSWYGIPRLEKIIQVGNRIKFVIKRPELLTHSTTEVTQPRTNTPVKEDMNV
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GIPRLERIVRGSNKIKFVVKKPELVISYLPPGMASKINTKALQSPKRPRSPGSNSKVP
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FNEKCGEALGLKQAVKVPFALFESFPEDFYVEGLPEGVPFRRPSTFGIPRLEKILRNK
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20081 20109,24648 24702,25874 25917,30516 30593,
34336 34345,51373 36429,38357 38419,48276 48386,
49719 49789 55737 52153,53415 53473,54953 55024,
55992 56175,57537 57595,62939 63010,64249 64432,
65374 65432,65828 65902,67505 67606,68515 68580,
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//gene="match to AF035737 (PID:g2827180); H_DJ0771P04.1"
//codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="general transcription factor 21"
/protein_id="AAD15419.1"
/db_xref="GI:4263747"
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                                                                                                                                                                                                                                                                                                                                                                                           /note="match to EST 239110 (NID:g561502)"
                                                                                                           /note="match to EST T06057 (NID:g317206)"
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/note="similar to EST AI346557
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0; Mismatches
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/rpt_family="L1"
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8610. .78320
/gene="GTF21"
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/gene="GTF21"
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Best Local Similarity 99.88
Matches 3292; Conservative
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atta 180 ATTA 91661 tcag 240 TCAG 91721 CCCG 300 	ccat 360 crcar 91841 qaqaq 420 qadaG 91901 	gaa 540 	Arcra 92141 cactc 720 cactc 720 cactc 92201 cagtc 780 cactc 92261 cagta 840 ctaga 840 ctaga 840	900 9238 9244 9244 9250	cctg 1080 ccrG 92558 aggt 1140 ccat 1200 ccat 1200 CcAT 92678
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121 9 91602 G 181 a 91662 A 241 9 91722 G	301 c 91782 C 361 ga 91842 G 421 ac 421 ac	481 t 1962 T 541 c 2022 C 601 g	92082 G 661 a 661 a 721 a 721 a 92202 A	841 9 2322 0 901 0 2382 0 961 9	1021 a 92502 A 1081 t 92559 T 1141 t 92619 T
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۵	Db 92679		92737
0 1	126	gaccatcotgggcaacatagcaggaccctgtctgtacaaaaaaattaaaaaatttaac	320
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a	162	tgacatttgagcagagaaatggaggagattatggagggaagatggtgaatgggggaac	1680
Ω	360£6 qa	GACATTTGAGCAGAGAAATGGAGGAGAGTTATGGAGGGAAGATGGTGAATGGGGGAAC	93157
O.	0y 1681	aaatg	1740
۵	Db 93158	TGGTCAAGACCAGGAATATGGTCAAGGGGGGAAAGATGGTCAAGGGGAACGCAGCAAATG	93217
a	174		800
Δ	Db 93216	AAAGGCCCTGAGGCAGGAGCAGCTTGATTCACCCCCAAAACCCGTGGGGCCCGTGCAGG	93277
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D	DD 93278	GACGGGAAGGACAAGTGTAAACCCTTTTCCTTGTCCCTGCAGGTGTGTGT	93337
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o	Qy 1921	gcctttctgtacctccctgcccctgtcccgaccgcgacaaaagcgacttccttt	1980
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<u>о</u>	Db 93518	GGGACACCTTCATCCGTCACATCGCCCTGCTGGGCTTTGAGAAGCGCTTCGTACCCAGC	93577
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Ω	3E9E6 qa	GGCCACCCTTGCAGTCCCAGGGCCAACCAGCTCCAGTGAGGACTAACGGGGCAGGGTCT	93697
0 1	222	tgggcacctggtccctggtctttgagcctggatctacccctctgatccctgggaagacag	280
1	0	1000CACC1CC1CC1CC1C1T1CACCC1CCACCCCCCCCCC	'n
a	Qy · 2281	1 ttcctttggaccgccctgggcccagccctttactgtcccgcctgtgcccagccag	2340

Craniata; Vertebrata; Euteleostomi;

Homo sapiens Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;

Catarrhini; Hominidae; Homo

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                                           geteteteaggteegaggeeeacteeteeaggaageetteeetgaetageeeagetatea
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DNA PRI 20-JUL-2000 7 BAC Clone 239c10, complete sequence.

AC004166 275197 bp Homo sapiens Chromosome AC004166 AC004166.12 GI:8887011

DEFINITION

AC004166

RESULT

ACCESSION

VERSION

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5
                                                                       2 (bases 1 to 275197)
Burian.D.M. and Roe,B.A.
Burian.D.M. and Roe,B.A.
Direct Submission
Submitted (21-FEB-1998) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
                                                                                                                                                                                                                                       Roe, B.A.
Direct Submission
Submitted (01-JUL-2000) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
                                                                                                                                                                                                                                                                                                                                   4 (bases 1 to 275197)
Ren,O., Buzian,D., Huang,E., Meadows,S., Korenberg,J. and Roe,B.A.
Direct Submission
Submitted (20-UUL-2000) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
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Burian,D.M., Ren,Q., Meadows,S., Huang,E., Korenberg,J. and
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                           E., Meadows, S., Korenberg, J. and BAC Clone 239c10
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On Jul 1, 2000 this sequence version replaced gi:8779478
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                                                               JOURNAL
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AUTHORS
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JOURNAL
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AUTHORS
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AUTHORS
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Matches 3213; Conserv
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I (bases I to 17302)
Chanock, S. J., Roesler, J., Zhan, S., Hopkins, P., Lee, P., Barrett, D.T., Christensen, B.L., Curnutte, J.T. and Gorlach, A. Blood Cenomic structure of the human p47-phox (NCF1) gene Blood Cells Mol. Dis. 26 (1), 37-46 (2000)
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Submitted (08-SEP-1999) Pediatric Oncology Bran. NIH/10/130240, Bethesda, MD 20892, USA
1. 17302
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL MEDLINE

AUTHORS

PUBMED REFERENCE JOURNAL

TITLE

DEFINITION

AF184614 LOCUS

source

FEATURES

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC092405 184558 bp DNA HTG 04-JUL-2001
Paplo cynocephalus anubis clone RP41-170F23, WORKING DRAFT
SEQUENCE, 6 unordered pieces.
AC092405. GI:14595779
                                                                                                                                                                                                    caccaccacgcctggctaatttttgtatttttagtagagacagggtttcaccatgttggc
                                                                                                                              2817 CACCACCACGCCTGGCTAATTTTTGTATTTTTAGTAGACAGGGTTTCACCATGTTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3073 agtggtgcgatcatagttcactgcagcctcaacctcccaggcccaagtgatcctcctgcc
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Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
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Consensus quality: 178116 bases at least 040
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (04-JUL-2001) NIH Intramural Seq
Grovemont Circle, Gaithersburg, MD 20877,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www.nisc.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: nisc_mouse@nhgri.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -- Project Information
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Center clone name: 170F23
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2 (bases 1 to 184558)
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SOURCE
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Db 155589 TACTAAAAATACAAAATTAGCCGGGCATGGTGGTGCACACCTGTAATCCCAGCTACTCGG 155530
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                                                                                                                                          NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 184558;
                                          Insert size: 168000; agarose fp
Insert size: 184058; sum-of-contigs
Quality coverage: 10.52x in Q20 bases; agarose-fp
Quality coverage: 9.60x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                  13928: gap of unknown length
31257: contig of 17329 bp in length
31357: gap of unknown length
42895: gap of unknown length
42895: gap of unknown length
61486: contig of 18591 bp in length
61586: gap of unknown length
111539: contig of 50053 bp in length
111739: gap of unknown length
111739: gap of unknown length
11858: contig of 72819 bp in length
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Consensus quality: 179898 bases at least Q30 Consensus quality: 181141 bases at least Q20
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/db_xref="taxon:9555"
/clone="RP41-170P23"
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13929. .31257
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31358. .42795
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/note="assembly_fragment"
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/note="assembly_fragment"
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1. .184558
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Best Local Similarity 81.4%;
Matches 2976; Conservative (
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53	GCAGCTTGGTTCACCCCCAAAATCCATGGGGCCCCATGTAGGCGACAGGAAGGA	153438	qq
1819	gcagcttgattcaccccaaaacccgtggggccgt	1760	Qγ
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153558	GGCGACAGAGCGAGACTCCGCCTCAAAAAAAAAAAAAAA	153617	DP
1644		1645	Οy
153618	CGGGAACCCGGGAGGCGGAGCTTGCAGTGAGCCGAGATCGCGCCACTGCACTCCAGCCTG		qq
1644		1645	Qy
153678	CCGGGCGTGGTGGCGCCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAGGAAATGG	153737	Dp
1644		1645	Qγ
153738	TCGAGACCATCCTGGCTAACACAGTGAAACCCCGTCTCTACTAAAAATACAAAAAACTAG	153797	qq
1644		1645	Qy
153798	TCAAGCCTGTAATCCCAGCACTTTGGGAGGCCGAGACGGGGGGGG	153857	QQ
1644		1645	Qγ
153858			qq
1644	ggcttctcggaagaggtgacatttgagcagagaaatggag		Qγ
153918		7	QQ
60	adacaaaaaaactgagaaaqqtatgaggtttgctatgcgatgtgaagttatcaag	154	ò
153978		154037	qq
1544	aagaaaattaaatgcaatttgcgatgcatcagtgataagtgctctgcagaaaag	14	δy
154038			Op
1487	geacttaagectggataacaaageaagacetgteteaaataacaatageaataat	1428	Qγ
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I bases 1 to 8119)
Gorlach,A. Lee,P.L., Roesler,J., Hopkins,P.J., Christensen,B., Green,E.D., Chanock,S.J. and Curnutte,J.T.
A p47-phox pseudogene carries the most common mutation causing p47-phox deficient chronic granulomatous disease
J. Clin. Invest. 100 (8), 1907-1918 (1997)
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/note="Human genomic EMBL3A bacteriophage clone L14 is a p47-phox pseudogene which is defined by the presence of GT deletion at the beginning of exon 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dorlach, A., Lee, P.L., Roesler, J., Chanock, S.J. and Curnutte, J.T. Borlach, A., Lee, P.L., Roesler, J., Chanock, S.J. and Curnutte, J.T. Direct Submission
Submitted (18-JUN-1996) Molecular and Experimental Medicine, The Scripps Research Institute, 10550 N. Torrey Pines Rd., CAL 1, La Jolla, CA 92037, USA
Location/Qualifiers
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gatectectgeeteageeeettgagtagetggggetacagggegeacaccaccatgeetgg 3180
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Characterization of the genomic structure of the p47-phox gene
                                                                     HS47L14S01 8119 bp DNA PRI 07-JAN-1998
Homo sapiens p47-phox (NCFI) pseudogene, clone L14, exons 1-5
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ÕM X	Query Match 63.8%; Score 2106.8; DB 9; Length 8119; Best Local Similarity 99.6%; Pred No. 0; Matches 2133; Conservative O. Mismatches 7: Indels 2: G		QQ	102
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QQ	18	40	qq	126
δ	1400 g	1459	δλ	247
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Christensen,B., Curnutte,J.T. and Gorlach,A.
Genomic Structure and the Identification of Multiple Polymorphisms
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Catarrhini; Hominidae; Homo.
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Gorlach, A. Lee, P.L., Roesler, J., Hopkins, P.J., Christensen, B., Green, E.D., Chanock, S.J. and Curnutte, J.T.
A p47-phox pseudogene carries the most common mutation causing p47-phox deficient chronic granulomatous disease
J. Clin. Invest. 100 (8), 1907-1918 (1997)
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Submitted (09-MAY-1996) P. Lee, Molecular and Experimental
Medicine, Scripps Research Institute, 10550 North Torrey P.
La Jolla, CA 92037, USA
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Gorlach,A., Roesler,J., Christensen,B., Chanock,S.J.
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                                                                                          caggaccetgtetgtacaaaaaattaaaaaatttaaccgggcatggtggcacacacc 1340
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in myeloid cells

ctr, 7703

2 (bases 1 to 3074)
Li,S.-L., Valente,A.J., Zhao,S.J. and Clark,R.A.
Direct Submission
Submitted (09-MAY-1997) Medicine, U. of Texas Hlth Sci (Floyd Curl Drive, San Antonio, TX 78284, USA
Location/Qualifiers
1. 3074
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source

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Alto)

promoter

gene mRNA

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Euteleostomi;

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, E Mammalia, Eutheria, Primates, Catarrhini, Hominidae,

Homo sapiens

ORGANISM

REFERENCE AUTHORS TITLE

JOURNAL MEDLINE REFERENCE

TITLE JOURNAL

AUTHORS

human.

KEYWORDS

SOURCE

1 (bases 1 to 3074) Li,S.L., Valente,A.J., Zhao,S.J. and Clark,R.A. 90.1 is essential for p47(phox) promoter activity J. Biol. Chem. 272 (28), 17802-17809 (1997)

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3051. 3071

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                                                                                                     Length 3074;
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Pred..No. 0;
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Homo sapiens cytosolic phagocyte oxidase protein (p47phox) gene, promoter region and partial cds.

AF003533.1 GI:2197080

10

RESULT 1 AF003533 LOCUS

DEFINITION

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Dp	1403	GACCTTGAATGAGCTCCAAAAGCTCTGGGCCTCCCAGGCTCTAGGGGGAGTGGGGAGAGAG 1462	Š
QY Db	421	aggecteagectglecctgggeatgetgecectecteacetetttgteceaaateceet 480 	3 8
Qy Db	481	tcctggcaaagctgacagtcttaatatcactctggagaaaactgagtcagccctaaggaa 540 	G G
QY Dp	541	caattcaatgaaccatttgcttacttgaggattggaactcaagtctcactca	cy Dp
Qy	601	gccattttcgtcccagctgtcactggcctcatccacacaca	b Cy
Qy	661 1703	acgettgcatgcacactcccatgcccggttcattcattcattca	or or
QY Db	721	attcattgactcattcattcattcactcactcattcactcagtgaatgttgcagtc 780	D C
QY	781	acgateceaatatttatggcetetgtgtgceaggcactagatggagggetgggggttaga 840 	da S
Qy	841	gccctgataacccggtcatgccctagctttcctgggacacattgtggtaaggggaga 900	ob Dp
Qy	901	ctaaaaaattaagtcaggccaggcacggtggctcatgcctgaatcccagcactttggga 960 	D CY
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QY	1081	taatoccagotaotoaggagactaacgcaagagaattgcttgaacccaggaggcagaggt 1140 	2
Qy Dp	1141	tgcggtgagccgagatcgcgccattgcactccagcctgggaaacaagagcgagactccat 1200 	짂
Qy Db	1201	ctcaaaaaaaaaaagtgggaggcagaggcaggagatcactagaggccagtagtttga 1260 	R
Qy	1261	gaccatcctgggcaacatagcaggacctgtctgtacaaaaaattaaaaatttaac 1320 	
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 1965)
Chanock, S.J., Roesler, J., Zhan, S., Hopkins, P., Lee, P., Barrett, D.T., Christensen, B.L., Curnutte, J.T. and Gorlach, A. Gonomic structure of the human p47-phox (NCF1) gene Blood Cells Mol. Dis. 26 (1), 37-46 (2000)
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1681 atggtcaagaccaggaatatggtcaaggggggaaagatggtcaagggggacgcagcaaatg 1740
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                                                                                                                                                                                                 2715 ATGGTCAAGACCAGGAATATGGTCAAGGGGGGAAAGATGGTCAAGGGGACGCAGCAAATG
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2 (bases 1 to 1965)
E 2 (bases 1 to 1965)
S Chanock, S.J., Roesler, J., Zhan, S., Hopkins, P., Lee, P., Barr Christensen, B.L., Curnutte, J.T. and Goerlach, A.
Direct Submission
Direct Submission
NIH/10/13N240, Bethesda, MD 20892, USA
INH/10/13N240, Bethesda, MD 20892, USA
I. 1965
II. 1965
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II. 1965
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Homo sapiens p47-phox (NCF1) pseudogene, partial sequence.
AF184613
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which is defined by the presence of a GT deletion at the
beginning of exon 2."
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1 (bases 1 to 1569)

Gorlach, Lee, P.L., Roesler, J., Hopkins, P.J., Christensen, B., Green, E.D., Chanock, S.J. and Curnutte, J.T.

A p47-phox pseudogene carries the most common mutation causing b47-phox - deficient chronic granulomatcus disease
J. Clin. Invest. 100 (8), 1907-1918 (1997)
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                                                                                                                                                                                                                                                                                                                  Mammalia: Butheria: Primates: Catarrhin; Hominidae; Homo.

(bases 1 to 7258)
Gorlach,A., Lee,P.L., Roesler,J., Hopkins,P.J., Christensen,B., Green,E.D., Chanock,S.J. and Curnutte,J.T.

A p47-phox pseudogene carries the most common mutation causing p47-phox deficient chronic granulomatous disease
J. Clin. Invest. 100 (8), 1907-1918 (1997)
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Gorlach,A., Lee,P.L., Roesler,J., Chanock,S.J. and Curnutte,J.T.
Direct Submission
                       1381 TTATCCTCTCCAGTAGGGTGACACCATGACAGGGGCCAATAGAGTCCTCCCATCTGTCCC 1440
                                                                                                                                                                                                                                                                                                                                                                                                                                              Chanock, S.J., Roesler, J., Hopkins, P.J., Lee, P.L., Bassett, D.T., Christensen, B., Curnutte, J.T. and Gorlach, A. Genomic structure and the identification of multiple polymorphi in the p47-phox gene Unpublished
                                                                                                                                                                                                                 PRI 07-JAN-1998 pseudogene, clone P43, exons 1-5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (17-JUN-1996) Molecular
Scripps Research Institute, 10550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Pl clone P43"
/chromosome="7"
                                                                                                                                                                                                         HS47P43S01 7258 bp DNA
HOMO Sapiens p47-phox (NCF1)
U60970
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/gene="NCF1"
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/gene="NCF1
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Pred. No. 0;
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1 (bases 1 to 7528)

Gorlach,A., Lee,P.L., Roesler,J., Hopkins,P.J., Christensen,B., Green,E.D., Chanock,S.J. and Curnutte,J.T.

A P47-phox pseudogene carries the most common mutation causing pay7-phox- deficient chronic granulomatous disease
J. Clin. Invest. 100 (8), 1907-1918 (1997)
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                                                                                                                                                                                                                                                                                                                                                                        HS47P40S01 7258 bp DNA PRI 07-JAN-1998
Homo sapiens p47-phox (NCF1) pseudogene, clone P40, exons 1-5.
U61238
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N. Torrey Pines Rd., CAL 1,
901 ATTITTAGIAGAGACAGGGITTCACCATGTTGGCCAGACTGGTCTCAAACTCCTGACCTC
                       2979 aagtgatccaccacctgggcctcccaaagtgctgggattacaggcatgagccaccgtgc
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                                                 961 AAGTGATCCACCCACCTGGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACCGTGC
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Scripps Research Institute, 10550
Jolla, CA 92037, USA
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Gorlach, A., Lee, P.L.,
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Pred. No. 0;
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/gene="NCF1"
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/gene="NCF1"
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Gorlach,A., Lee,P.L., Roesler,J., Christensen,B., Chanock,S.J. and
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Gorlach, Lee, P.L., Resler, J., Hopkins, P.J., Christensen, B., Green, B.D., Chanock, S.J. and Curnutte, J.T.
A p47-phox pseudogene carries the most common mutation causing p47-phox deficient chronic granulomatous disease
J. Clin. Invest. 100 (8), 1907-1918 (1997)
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Chancek, S.J., Roesler, J., Hopkins, P.J., Lee, P.L., Bassett, D.T.,
Christensen, B., Curnutte, J.T. and Gorlach, A.
Characterization of the genomic structure of the p47-phox gene
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Claim 12; Fig 11A-JJ; 87pp; English.

The present sequence represents the human musashi promoter, which is used in the method of the invention. The specification describes a method for separating multipotential neural progenitor cells from a method for separating multipotential neural progenitor cells from a conclusic acid encoding a fluorescent protein under control of a promoter which selectively functions in the progenitor cells, into all cell types of the mixed population, allowing only the progenitor cells to express the fluorescent protein, and identifying and separating cells that are fluorescent, where the separated cells are progenitor cells. The method is useful for isolation and purification of multipotential correctly progenitor cells, especially neural stem cells from adult brain. The isolated cells are used in both basic analyses of precursor and stem cell growth control, as well as in more applied studies of their cransplantability and engraftennt characteristics. The cells are useful in support of the structural repair of the damaged central nervous system, such as in the traumatized brain, or the contoured, traumatized or transected spinal cord.

Sx Sequence 52216 BP; 13494 A; 12461 C; 12362 G; 13899 T; 0 other;

22; 11688 GCCGGGCACGGTGTCTCATGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGTGGAT 11629 AAAAATATAAAAATTAGCTGGGCATGGTGGTGTGCCCTATAGTCCCAGCTACTTGGGAG 11511 A---AAAAAAGTCCTGGTGCGGTGGCT-GACGCCCGTAATCCCAGCACTTTGAGAGGCC 11335 TCCGTCTCTACTAAAAACACAAAACTTAGTTGGGCATGGTGGCGTGTGCCTGTAGTCCCA 11217 358 418 470 650 184 244 Gaps 65 agttgggaaaaggccaggtgcagtggctccacgcctgtaatcccaacactttaagaggct gctgtgatcacgtcactgtactctagcctgggcaacagagcaagactctgtctccaaaaa 6 gtcaggcactgtggctcatgcctgtaatcccagcactttgggaggccgaggcggttgaat aaaaatacaaaaattagccaggtgtggtggtggcgggtgcttgtagtcccagctacttgggag gctgaggcaggtgaattacttgaacctgggaggtggaggttgcaatgagccaagattgca gaggtgggagaatcctttgagcccaggagttcgagaccagcctgggcattgtcccaagac gctattcgggaggctgaggcagggagattgcttgagcctaggagtctagggctgtagtga agaaaattaaagttgggaaaggctcactaacttcatcagatgagaacaaagacatgtttga cttgtctttacaaaaaa-----ttagccgggtgtggtggcatacgtctgtggtccca 166; Score 406; DB 22; Length 5 Pred. No. 3.4e-83; 0; Mismatches 1015; Indels 12.1%; ilarity 54.3%; Conservative Local Similarity Matches 1401; Query Match Best Local 5 419 299 11096 11570 245 11390 11276 99 125 185 359 11216 531 11628 471 11156 591 qq g qq Dp à g ŏ g à QQ ò q ò qq ŏ qq ò qq δ ò ò ŏ

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AAAAATAGATATAGGCTACTTGGGAGGCTGAGATGGGAGGATCACTTGAGCCCAAGAGG- 10062 GAGATCTCTGCTCACTGCAACCTCCGCCTCCAAAGTTCAAGCGATTCTCCTGCCTCAGCC 10813 ---TTTCACCATGTTGGATTACAGGTG 10717 10597 -----AAAATTACAAATGTAACAT 10293 AAAAAGTAAAAAGTTCTTTACCCCTTAGACTCCTTCCCTAAATGTAACTGTTACCAATTTC 10183 caggitiggiggitcigicagaigaaagcaaagcgaggciggaicccagcaiccticcig 1430 teggetetggetttgggggeeetggeaggttgtgatgeee--ttggtctggacagggaace 1668 aggaggaggagcagactcgggagagtgggaggccagtggtgtctgtggatatgtggc 1728 tecagetetgttagggggeetaaatgteeteeeacactgtgggtegeettetettag 1070 <u> ACAGGCGCCTGCCACCACCCCCGGCTAATTTTTGTATTTTTAGTAGAGATAGAGTTTCAC</u> CAATGTGTAGG-----GATTACAGGCATGAGCCACTGCATCCAGCCCTAAACCACAT GTGCTCACA-----TTAAAAGAAAAAAATGCGTCAGTACACAAAGGTATAAGATG ATGTATATCCTTCCAAAAATGTTCCATGCCTATATACTTAGATATGATTATATTATTA AACCTCTGCCTTCCGGGTTCAAACAATTCTCCTGCCTCAGGCTCCCAAGCAGCTGGGATG ctgatggctgcagggagccgctgggccctgccctcagtcacattcccgcacctctggca caagatgccagcgcctgttctggaggcccagatgggccctgcaatgcccactcacctgc TITGGTTTTTTTTTTGAGATGGAGTCTTGCTC - - - TGTTGCCAAACTGGAGTGCAGTGG cgactacgagaagacctcgggctccgagatggctctgtccacgggggacgtggtggaggt cgtggagaagagcgagagcggtcagacctcccaccttacggggctccttcccctggtgct 10812 TCCTGAGTAG-CTGGGACTACAGGTGCGCCTCACCATGCCCAGCTAATTTTTATATTTTT caggaacccacagaccacaagccccctgccaaggctcaggcagcctggcccctgggaggac AAAACCACATITCTITIGITITGTITITIGAGACAGAGICTIGCTCGTCACCCAG cgtgttctgtctggatggggtatgggaccgtctgttcattatgaagtgggctcagagctgt gattctgtgagcatgtgtgcatgcatgcatgtgacctcattgtccagtgtggaggtg acatttocaaatctgagcattggacatcagtgtgtctgtgtccctgtgtcctcaccatcc agcccctggacagtcctgacgagacggaagaccctgagcccaactatgcaggtgcccct gactgctttggagtctgggctggttgctggcttggcagaaaagtcagggctaagatctca cetecetettgececagacateaceggececateatectgeagaegtacegegecattge 10330 TTCTATTAGCTAGTTTTTA-----ATTAAAATGTTAATA - - -AGTAGAGACAGGG-1011 1131 1191 1311 1371 1431 1611 1669 711 771 10562 1251 1551 10242 11036 10988 10928 951 10753 10716 10596 10502 10442 10382 1491 10292 10182 10122 q Db Dp qq qq qq g q QQ qq g Ωp δŏ q Db qq Dp q QΥ Qγ δλ $^{\circ}$ Óλ δ Qγ Qγ δ δy δŏ öλ δy δy QΥ Óλ Qγ

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Ruben SM;

Barash SC,

Rosen CA,

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number of colorectal cancer antigens. These are shown in AAI57547-AAI57619 and AAM38569-AAM38641. These can be used in the diagnosis, prevention and treatment of cancer of the colon and/or rectum. The present sequence is a colorectal cancer antigen genomic sequence. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                preventing and/ or prognosing rectum including colorectal cancers
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Pred. No. 6.5e-80;
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                                                                                                                                            present invention provides the protein and coding sequences of oelorectal cancer antigens. These are shown in
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    gttgggaaaaggccaggtgcagtggctccacgcctgtaatcccaacac

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                                                                                                               Disclosure; SEQ ID NO: 328; 522pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                  Sequence 32152 BP; 8332 A; 7335 C; 7256 G; 9229 T; 0 other;
                                                                                and also for testing and detection e.g. diagnosis
                                              for treating,
the colon and
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52.3%;
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Best Local Similarity 52.3
Matches 1403; Conservative
                                              Isolated polypeptide disorders related to
             WPI; 2001-457727/49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65
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QQ	29504	CACGAATCCCTTACTGTTAGACATTTTGATTTGCCACTTTATCACTGTTATACATGGAGC	29445
Qγ	741	gatgggcctgcaatgcccactcacctgccctcttgccccagacatcaccggccc	800
QQ	29444	GATGCTCCCAGCTTGAGTTTAAGAAGAATTCAGACCTGCCAGGAGCCTCTGTAAAGAGCC	29385
Οy	801	catcatcctgcagacgtaccgcgccattgccgactacgagaagacctcgggctccgaga-	.859
Op	29384	TAGGGAGGCCAGACGCCGTGGCTCACGCCTGTAATCCTAACACTTTGGGAGGCCGAGAC	29325
Οy	860	tggctctgtccacgggggacgtggtggaggtcgtggagaagagcggtcag	915
Op	29324	AGGCAGATTGTCTGAGCTCAGGAGTTTGAGACCAGGCCAGGGCAACACGGCGAAACCCCGT	29265
οy	916	acctcccaccttacggggctccttcccctgqtgctcaggaacccacagccacaagcccc	975
QQ	29264	CTCTACTAAAATACAAAAAAGTAGCGGGCGTGGTGGTGGTGCTGTAGTCCCAGCTAC	29205
ΟŶ	916	tgccaaggctcaggcagcctggccctggaggactccagctctgttaggggccctaaat	1035
qq	29204	TCGGGAGGCTGAGGCAGGAGAATTGCTTGAACCCGGGAGGCGGAGGTTGCAGTGATCCAA	29145
οy	1036	gtcctcccacactgtgggtcgccttctctcttagtgtgcaccctgtggtggctgtgggc	1095
qq	29144	GATCGCACCACTGCACTCCAGCTGGGTGACAGAGCGAGACTCCCGTCTCCAAAAAAA	29087
οy	1096	atctgtgcatggcaggccggggggggggggtctgcggtgttctgtctg	1155
qq	29086	AAAAAAAGCCCAGGGCAGACTGCAAGAAGCCCACATGCAGGGGGGGG	29027
ογ	1156	gtgattctgtgag	1203
Op	29026	CAGCTCAGGTCATCCTAGGGAAAACTCTTAGCTGCTCCATGGAACAGGTGACTGAGTGCCA	28967
ογ	1204	tgtgtgcatgcatgcatgtgacctcattgtccagtgtggtggaggtgacatttccaaatc	1263
QQ	28966	TCAGAGTTAGGGAGAGGGTGGGGGGGAAATTATTCCTCAGTTTGTCTCCAGGTGCAT	28907
δy	1264	tgagcattggacatcagtgtgtctgtgtccctgtgtctcaccatccctgatggctgcag	1323
QQ	28906	CCCCCTGTAGACTTAAGCCCCCCACAGAGAGATGGGTAGCATAACAAGTGAAAGAACCAA	28847
Οy	1324	ggagccgctgggccctcagtcacattcccgcacctctggcacaggttggtgt	1383
qq	28846	GTCGGGGATTGTGGCTGGTGCTGTAGTCTCAGCTTGGGAGGTTGGGGTGGGAGGAT	28787
Qy	1384	ctgtcagatgaaagcaaagcgaggctggatcccagcatccttcct	1440
q	28786	GGCTTGAGCCCAGGAGTTTGTGTCTGCCTGGGCAACACACGCTTTATTAGGAAAAAGGGA	28727
οy	1441	cagtcctgacgagacggaagaccctgacccaactatgcaggtgcccctgccctccgag	1500
qq	28726	AGGGAAGGGAAGGGAAGGAAGGAAGGAAGGAAAAGAAAGGAAAA	28667
ογ	1501	gctgtaggggtgtgggagaaagggcaggcaggg	1538
QQ	28666	AGAGAGTGAGAGAAAGAAAGGAAGGAAGGAAGGAAGGAA	28607
ογ	1539	gggatattgagtgactgctttggagtctgggctggttgctggctg	1598
qq	28606	GGAAAGGAGGAGGAGGAGGAGGAGGAGGAAGGGAAGGGAAGGGAAGGGAAG	28547
Qγ	1599	gctaagatctcatcggctctgggttgggggccctggcaggttgtgatgcccttggtctgg	1658
Op	28546	GGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAAGAAAA	28487
Οy	1659	acagggaaccaggaggaggagcagacgactcgggagagtgggaggccagtggtgtctgtg	1718
Dp	28486	AGAGGAAAGAAGAAGAAGAAGAAGGGGAGGAGAAAAAGGAGA	28427
ογ	1719	gatatgtggccaggttcagtgggaagctgaaggatgagcagaccttaggctcaggaagga	1778

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Human neuroblastoma cell line NB-1 1p36 nucleotide sequence SEQ ID NO:60.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; chromosome 1; 1p36; neuroblastoma cell line; NB-1; anticancer; tumour suppressor; human 1p36 homozygosity deletion domain; tumour;
                                                                                                                                                                           tctgtcacccaggctggagtgcagtaatgcaatctcagctcactgcaaccttagcctcct
                                                                                                                                                                                                                                                                                                                                                                        gctggtctcgaactcctgacctcaggtgatccgccgccttggcctcccaaagtgctagg
                            gggctgcctggaagtgggggatcatcattaccagaaagggaaaactggcagtg....
                                            ------ccagggctggatggggcctgcattgagcttgaaaaaactataataga
                                                                                                             28246 TITGGTTTTGGGGTTTTTTTTTTTTATTTTTTTTTTTAAATTTTCTTTGAGATGAAGTCT
                                                                                                                                       1942 cactcccttgctaaggctggagtgcggtggtgctatctcagctcactgcaacctctgcct
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ID AAF97846 standard; DNA;
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                                                                                                                                                                                                                                                                                                                                   The present invention describes a homozygosity deletion domain co-existing in the 36-position of the first chromosome short arm (1p36) in human neuroblastoma. Also described are base sequences from the 1p36 position of human neuroblastoma cell lines (NB-1 and MASS-NB-SCH-1), which are tumour suppressor genes in human neuroblastoma. The genes are tumour suppressor genes in human neuroblastoma. The genes are tumour suppressor genes, base sequence data of which are applicable as tumour markers and reagents in studying mechanism of tumour body formation, and gene diagnosis of tumours as well as in developing anti-cancer drugs. ARF97787 to ARF9782 represent PCR primers used in the exemplification of the present invention, and AAF97830 to AAF97874
                                                                                                                                                                                                                                            Human 1p36 homozygosity deletion domain from the 36-position of first chromosome short arm in human neuroblastoma cell lines, applicable e.g. in gene diagnosis of tumors as well as in developing anti-cancer drugs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46314 TITATIGICICIATOTATOTATOTATITITICAGACGAAGICICACIOTIGICCCOTAGG 46255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 385.8; DB 22; Length
Pred. No. 1.5e-78;
0; Mismatches 152; Indels
                                                                                                                                                                                                                                                                                                            8; Page 67-88; 226pp; Japanese.
                                                                                                                                                      (HISM ) HISAMITSU PHARM CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.5%;
76.9%;
                                                                                       31-AUG-2000; 2000WO-JP05930
                                                                                                                31-AUG-1999; 99JP-0245962
09-MAY-2000; 2000JP-0136266
                                                                                                                                                                   (CHIB-) CHIBA PREFECTURE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      522; Conservative
                                                                                                                                                                                                                    WPI; 2001-226686/23.
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Best Local Similarity
Matches 522; Conserv
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              Homo sapiens.
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The present invention describes a method for detecting a genetic mutation in the yes! gene for the diagnosis of a yes! mediated neuropsychiatric disorder in a human. The method comprises detecting the presence or absence of a genetic mutation in the yes! gene of the presence or absence of a genetic mutation in the yes! gene of the calletion and results in the production of a bys! protein having an amino acid sequence other than the wild type yes! amino acid sequence and the presence of the genetic mutation identifies a subject that has or is at risk for developing a yes! mediated neuropsychiatric disorder. Compounds that bind to the yes! gene product, are useful for treating a yes! mediated neuropsychiatric disorder. The disorders include Huntington's disease, and especially bipolar-affected disorder. (BAD) also known as bipolar mood disorder (BP) or manic-depressive
                                                                                                                                                                                                                                                                                                                                                                               45658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      schizophrenia;
ctgacctcaggtgatccgcccgccttggcctcccaaagtgctaggattacaggtgggaac
                                                                                                                                                                                                     ttttttgtatttttagtagagatggggtttcgccatgttggccaggctggtctcgaactc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; yes1, diagnosis, neuropsychiatric disorder; BAD, bipolar affective disorder; attention deficit disorder; schizoaffective disorder; unipolar affective disorder;
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P-PSDB; AAY24421.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          illness. The method distinguishes neuropsychiatric disorders from neurological disorders, which enables more accurate evaluation and prescription of medical treatment. The present sequence represents human yesl cDNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse; tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
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                                                                                                                                         agata-gagteteaeteeettgetaaggetggagtgeggtggtgetateteageteaetg
                                                                                                                                                                                                                                                                                                                                                                                          accttagcctcctgggttcaagcaattctcctgcctcagccacctgagtagcctggggtt
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                                                                                                                                                                                                                                                   caacctctgcctcccaggatcaagtgattctccagcctcagcctcccaggtagctggga
                                                                      Length 119950;
                                              other
                                             26
                                                                     Score 382.8; DB 20; Length
Pred. No. 9.7e-78;
0; Mismatches 162; Indels
                                            Sequence 119950 BP; 34471 A; 23730 C; 24660 G; 37033 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human EST-derived coding sequence SEQ ID NO: 650.
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                                                                       11.4%;
76.4%;
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                                                                                        Conservative
                                                                              Best Local Similarity
Matches 547; Conserv
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                                                                       Query Match
Best Local 9
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proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, from the organism of interest. They can be used in diagnostics, biodrensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a cDNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention provides the protein and coding sequences of novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                agagteteaete-eettgetaaggetggagtgeggtggtgetateteageteaetgeaae 1993
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diagnostics; forensic test; gene mapping; genetic disorder;
biodiversity; gene therapy; nutrition; ss.
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Pred. No. 1.2
                                                                                                                                                                                                                                                                                                                                                                                                                              Drmanac RA, Zhang J, Werhman T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polypeptide for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                           Qian XB,
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76.2%;
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17-JUL-2000; 2000US-0617746.
03-AUG-2000; 2000US-0631451.
15-SEP-2000; 2000US-0663870.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   research use
                                                                                                                                                                                                                                                                                                                                                                                                           Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 76.2
Matches 532; Conservative
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P-PSDB; AAM24134.
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                                                                                                                                                                                                                                                                                                                                                                                                         Liu C,
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                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                especially neuropsychiatric disorders e.g. BAD, schizophrenia, or HKNGI-mediated myopia disorders, such as early-onset autosomal dominant myopia. The polynucleotides can be used in gene therapy techniques to treat such disorders. They are also useful in diagnosis to identify individuals having, or at risk of developing, HKNGI-mediated disorders due to mutations in the HKNGI gene. Such mutations especially
                                                                                                2472
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                                                                                                                                                              cgcctcccaagttcaagctattctcctgcctcagcctcctgagtag-ctgggattacag
                                                                                                               2294 agtettggetetgt-cacceaggettggagtgeagtaatgeaateteageteaetgeaaeet
                       agetecgetetgtecgeecaggetggagtgeageggegateceggeteactgeaacet
                                               2353 tagcctcctgggttcaagcaattctcctgcctcagccacctgagtagcctggggttacag
                                                                                                 gcatgcaccaccacgccaggctaatttttgtatttttagtagagatggggtttcgccat
                                                                                                                                                  HKNG1; Hong Kong new gene 1; bipolar affective disorder; BAD; neuropsychiatric disorder; early-onset autosomal dominant myopia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New HKNG1 polynucleotides useful in diagnosis and treatment of neuropsychiatric disorders, e.g. bipolar affective disorders and
                                                                                                                                                                                                2533 agtgctaggattacaggtgggaaccaccttgcccagcc 2570
                                                                                                                                                                                                               Genomic sequence of the human HKNG1 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 2; Fig 3A-R; 205pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                              schizophrenia; splice variant; ss.
                                                                                                                                                                                                                                                                                    AAZ10752 standard; DNA; 72604
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98US-0106056.
99US-0236134.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US05606
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                                                                                                                                                                                                                                                                                                                                     23-NOV-1999
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28-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55102
result in the production of a protein with a different sequence to the human full-length HKNG1 polypeptide or splice variant sequences, especially the substitution of a lysine for a glutamic acid at residue 202 or 184. The polynucleotides are also useful in gene mapping, to produce probes or primers to identify similar sequences (e.g. mutants or sequences from different species) and to produce transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2148
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                                                                                                                                                                                                                                                                                                                                                                          1910 tttatttatttttacttttttgagatagagtctcactcccttgctaaggctggagtgcggt 1969
                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human SHOX (short stature homeobox containing gene) gene sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2089 ttttagttgagacggggtttcaccaggttggccagactggtctcgaacttctgacctcag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55103 ttttagtagagatggggtttcaccatgttggttaggctggtggcgaactcctgacctcaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55163 gigatitigectgeetetgeeteceaaagigetigggatiacaggegigageeaceatgeee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ggcctggttaccc---acattttaaaatggagtgatttcacccttttatgtggatttac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2265 agcttgttttttttttttttttgagacaaagtctggctctgtcacccaggctggagtgca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gtgatctgcctgcctcggcctcccaaagtgctggaattacagatgtgagccactgtccct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55223 agcccctttctccctttttaaatatcaccagcctgggttctttgtttttgttttgttt
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                                                                                                                                                                                                                                                                                                                        0; Mismatches 149;
                                                                                                                                                                                                                                                                          Score 373.2; DB 2
Pred. No. 1.3e-75;
                                                                                                                                                                                                 Sequence 72604 BP; 20579 A; 15146 C; 14859
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                                                                                                                                                                                                                                                                          11.18;
76.78;
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                                                                                                                                                                                                                                                                                                                          Conservative
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AAV35620/C
ID AAV35620 standard; DN
XX
AC AAV35620;
XX
DT 07-SEP-1998 (first e
XX
DE Human SHOX (short sta
                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                        Matches 521;
                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                    animals.
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This is the human SHOX gene sequence containing the PARI region. The gene region corresponding to short stature has been identified as a region of approximately 500 kb in the PARI region of the x and Y chromosomes. Three genes in this region have been identified as a chromosome. Three genes in this region have been identified as candidates for the shoxt stature gene. These genes were designated SHOX (also referred to as SHOX93 or HOX93), PET92 and SHOT (SHOX-11ke homeobox gene on chromosome three). The SHOX gene has two separate splicing sites resulting in two variations SHOXa and SHOXb. The specification provides sequences of SHOX (short stature homeobox-containing) genes SHOX shoxb, SHOX and exons of the SHOX genes as shown in AAV35610 to AAV3561 and protein sequences of the human growth protein transcription factor SHOXa, SHOXb and SHOT as shown AAW60573. The novel genes are responsible for human growth. Defects in the genes can cause short stature, e.g. Turner's syndrome. The products can be used to develop agents for the treatment of short stature or other human growth disorders. The products can also be used for providing a mitogenic effect or cells, e.g. for the treatment of bonc diseases such as osteoprosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and diseases involved with disturbance in the bone calcium regulation.
                 Homeobox domain; human growth gene; growth regulation; growth defect; turner's syndrome; short stature homeobox containing gene; SHOXa; SHOX; bone disease; osteoporosis; calcium regulation; short stature;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                  human growth genes - used to develop products for the diagnosis treatment of human growth defects such as short stature, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tggagtgcggtggtgctatctcagctcactgcacctctgcctcccaggatcaagtgatt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 370.6; DB 19; Length
Pred. No. 3.9e-75;
0; Mismatches 144; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 19; Pages 51-67; 84pp; English.
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76.2%;
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                                                                                                                                                                                                                                                                                                                  (RAPP/) RAPPOLD-HOERBRAND G.
                                                                                                                                                                                                                         97WO-EP05355
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                                                                        transcription factor A; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Turner's syndrome
                                                                                                           Homo sapiens
                                                                                                                                              WO9814568-A1
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01-OCT-1996;
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Best Local Si
Matches 513;
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Human; secreted protein; immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nonctropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; vulnerary; autoimmune disease; cardiovascular disorder; hyperproliferative disorders; cerebrovascular disorder; wound healing; nervous system disorder; ocular disorder; skin ageing; chemotaxis;
                                                                                                                                                                                                                                                                                                        10542 CTGACCTCAAGCGATCCACCTCCTGGGCCTCCCAAAGTGCTGGGATGACAGGCGTGAGC 10483
                                                                                                                                                     Nucleic acid.molecules encoding human secreted proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's Parkinson's diseases and cancers -
                                                    10482 CACTGCACCTGGCCTAGAACTGGAAAT------TGGGTTTTCTTTTTGATTT
                                                                                              ctgcctcagccacctgagtagcctggggttacaggcatgcaccaccacgccaggctaatt
                                                                                                                                                                                                            cactgtccctggcctggttacccacattttaaaatggagtgatttcacccttttatgtgg
                                                                                                                                      agtgcagtaatgcaatctcagctcactgcaaccttagcctcctgggttcaagcaattctc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0138630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2000; 2000WO-US14973
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          food additive;
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thuman secreted proteins AAB75506 - AAB75554 are encoded by polynucleotide sequences AAF64176 - AAB76424. The specification includes amino acid sequences AAB75555 - AAB750606 which represent fragments of the human secreted proteins, and protein sequences with which they share homology. The proteins and polynucleotides, their agonists and antagonists have activities dependent on the itssues and cells in which they are expressed, examples of these activities include, inwinosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; cy asotropt; cerebroprotective; notropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; and vulnerary. The proteins, virucide; fungicide; opthalmalogical; and vulnerary. The proteins, virucide; dispasses and disorders including, autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders cordiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease, angiogenesis, nervous system disorders e.g. Alzheimer's disease, can encebral infection. The polypeptides can also be used to aid wound hading and epithalial cell proliferation, to prevent skin ageing due to sunburn, to maintain organs before transplantation, for supporting cell collucase or decrease storage capabilities included in the invention are polypeptides can also be used as a food additive or preservative to prive used in the isolation, identification and characterisation of the proteins of the invention.
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Sequence 1298 BP; 386 A; 249 C; 293 G; 362 T; 8 other;

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                                                                                 tatttttatttatttattttattttattttactttttgagatagagtctcactcccttgctaa 1955
                                                                                                        1112 CTGATTTTTTTGTATATTTAGTAGAGGGGGTTTCMCCATGTTAGCCAGGATGGTCT 1053
                                                                                                                                                                                                                                                                                                                                                                                                              2133 gaacttctgacctcaggtgatctgcctgcctcggcctcccaaagtgctggaattacagat 2192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2313 ggetggagtgeagtaatgeaateteageteaetgeaaeettageeteetgggtteaagea 2372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ctaattttttgtatttttagtagagatggggtttcgccatgttggccaggctggtctcga 2492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2193 gtgagccactgtccctggcctggttacccacattttaaaatggagtgatttcaccctttt 2252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  879 GGYTGGAGTGCAGTGGCGCCATCTCCACTCGAAAGCTCCGGCTCCCGGGTTCAGGCC 820
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                                          14;
11.0%; Score 370; DB 22; Length 1298; 77.0%; Pred. No. 1.8e-75; tive 6; Mismatches 136; Indels 14;
                                          Conservative
                     Similarity
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Matches 522;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents the retinoblastoma binding protein-7 (RBP-7) genomic sequence of the invention. The RBP-7 coding sequence and progulatory sequences are useful for the recombinant production of the protein and for expressing heterologous nucleic acids. Primers and probes derived from the RBP-7 nucleotide sequence (e.g. AAZ87035-287099) are useful for DNA amplification and detection methods. RBP-7 biallelic markers (see AAZ86993-287034) are useful for diagnosis of disease related to alteration in the regulation or in the coding regions of the RBP-7 gene and for prognosis/diagnosis of an eventual treatment with therapeutic agents, especially agents acting on pathologies involving abnormal cell proliferation and/or differentiation, these include thyroid hyperplasta, psoriasis, benign prostate hypertrophy, cancers, including presst cancer, sarcomes and other neopleans, pages and cancer, and the concert of the concert of the concert of the cancer of the concert of
Novel nucleic acid and polymorphic markers used for diagnosis of diseases, especially those involving abnormal cell proliferation and differentiation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Retinoblastoma binding protein-7 genomic DNA sequence.
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                                                                                                                                                                                                                                                                                                                BP.
                                                                                                                                                                                                                                                                                                          AAZ86967 standard; DNA; 162450
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                                                                                                                                                                      642 GAGCCACCACGCCCAGCC 625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ttagcctcctgggttcaagcaattctcctgcctcagccacctgagtagcctggggttaca
                                                                 91815 GGGTCTTGCTCTGTCACTCAGGCTGGAGTGCTGTGGCACGGTCTCAGCTCACTGCAACCT
                                                                                                                                                                       gcatgcaccatgcctggataatttttgtatttttagttgagacggggtttcaccagg
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/note= "pET92 region (second part)"
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/*tag= b
/note= "pET92 region (first part)"
4326..4437
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/note= "part of exon I (G310)"
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WHOMEODOX domain; human growth gene; turner's syndrome; short stature how turner's syndrome; short stature how SHOX; bone disease; osteoporosis; c

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Homo sapiens.

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Key

Location/Qualifiers
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Acce A198.1807

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This is a preliminary nucleotide sequence of the SHOX gene. The gene region corresponding to short stature has been identified as a region of approximately 500 kb in the PARI region of the X and Y chromosomes.

Three genes in this region have been identified as candidates for the short stature gene. These genes were designated SHOX (also referred to as SHOX93 or HOX93), per92 and SHOT (SHOX-1ike homeobox gene on chromosome three). The SHOX gene has two separate splicing sites canculting in two variations SHOXa and SHOXb. The specification provides sequences of SHOX (short stature homeobox-containing) genes SHOX F192, SHOXa, SHOXb, SHOY and exons of the SHOX genes as shown in AAV35610 to AAV35621 and protein sequences of the human growth protein transcription factor SHOXa, SHOXb and SHOY as shown AAW60573. The novel genes are responsible for human growth. Defects in the genes can cause short stature, e.g. Turner's syndrome. The products can be used to develop agents for the treatment of short stature or other human growth disorders. The products can also be used for providing a mitogenic effect on cells, e.g. for the treatment of bone diseases such as osteoporosis
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/*tag= d
/note= "pET92 region (third part)"
5305..5512
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/note= "part of
11620..11729
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2000US-022526
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2000US-0225757
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2000US-0229513.
2000US-0230437.
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   Human; kidney antigen; immunosuppressive; antiarthritic; antirheumatic; antipolierative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmological; antiallergic; hepatotropic; antidiabetic; antiallammatory; antiulloer; vulnerary; anticonvulsant; antiparastic; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; ds.
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04-ARR-2000; 2
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17-MAR-2000; 2
19-MAY-2000; 2
19-MAY-2000; 2
20-JUN-2000; 2
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(AAIGS911-AAIG373) and the encoded polypeptides (AAM42417-AAM42691) collectively known as kidney antigens and the use of such kidney antigens for detecting disorders of the kidney, especially kidney cancer and kidney cancer metastases. The polynucleotides and proteins are also useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer, and other cancers of the adrenal gland, bone, bone marrow, breast, assertointestinal tract, liver, lung, or urogenital; (b) immune disorders
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(c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.

Note: The sequence data for this patent did not form part of the brinted specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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Prostate carcinoma antigen-1; PCTA-1; human; galectin-8 homologue; splice variant; prostate cancer; biallelic marker; polymorphism; detection; diagnosis; prognosis; drug screening; ds.
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This sequence represents the genomic DNA sequence encoding human prostate carcinoma tumour antigen-1 (PCTA-1). At least three PCTA-1 DNAA MAAN 10226, AAAN 10228, 
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Human; kidney antigen; immunosuppressive; antiarthritic; antirheumatic; antipoliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmological; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiuleer; vulnerary; anticonvulsant; antiparasitic; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; ds.
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     1940 ctcactcccttgctaaggctggagtgcggtggtgctatctcagctcactgcaacctctgc 1999
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(AAI63971-AAI6393) and the encoded polypeptides (AAM42417-AAM42691) collectively known as kidney antigens and the use of such kidney antigens for detecting disorders of the kidney, especially kidney cancer and kidney cancer metastases. The polyuclectides and proteins are also useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cencer, and other cancers of the adrenal gland, bone, bone marrow, breast,

invention relates to novel kidney related polynucleotides

(b) immune disorders

gastrointestinal tract, liver, lung, or urogenital; (b) immune disorde e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. crebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

parasitic infections.

Sequence 32134 BP; 8893 A; 6674 C; 6825 G; 9742 T; 0 other;

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New isolated nucleic acids and polypeptides, useful for diagnosing, treating and/or preventing human diseases and disorders $\,$ Ruben SM Barash SC, WPI; 2001-488784/53 Rosen CA,

Disclosure; SEQ ID NO 837; 564pp + Sequence Listing; English

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GST is a type 1 membrane protein useful for inhibiting a binding event between a selectin and a selectin ligand, which comprises contacting the selectin with a non-sulphated selectin ligand, GST and a small molecular agent that inhibits the sulphation activity of GST. GST is also useful in inhibiting a selectin mediated binding event. GST is useful in gene therapy to treat disorders such as acute or chronic inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         systemic lupus erythematosus (SLE), rheumatoid arthritis, polyarteritis nodosa, polymyositis, dermatomyositis, systemic sclerosis, diabetes, glomerulonephritis, myasthenia gravis, Sjogren's syndrome, Hashimoto's disease, Grave's disease, adrenalitis, hypoparathyroidism, pernicious anaemia, demyelinating diseases, cirrhosis, ulcerative colitis, segmeratis, ragional enteritis, adult respiratory distress syndrome, infantile eczema, posciasis lichen planus, allergic rhinitis, bronchial asthma, hypersensitivity, rheumatic fever and tissue rejection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches 991; Indels 204; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New glycosyl sulfotransferases (GST)-4alpha, GST-4beta and GST-6 for diagnostic and therapeutic agent screening applications
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aaaggtcaggcactgtggctcatgcctgtaatcccagcactttgggaggccgaggcggtt 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Portion of 5' untranslated region (5'UTR)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 160552 BP; 40281 A; 37573 C; 38015 G; 44564 T; 119 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 363.6; DB 22; Length 160552; Pred. No. 2.8e-73;
                                                                                                                                                                                                                                                                                                                                                                                /*tag= q
/note= "Includes 17 base pairs of 5'UTR, the ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product- "Human glycosyl transferase-4beta
                                                                                                     'cons_splice= (5'site:NO, 3'site:NO)
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                                                                                                                                                                                                                                                                                                                                                                                                                                            and all of 3'UTR"
98457..98473
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/label- 4a_502
83348..96412
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99662..99968
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                                                                                                                                        96413..96484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-JUL-1999; 99US-0144694.
13-JUL-2000; 2000US-0593828.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; AAY72639, AAY72640.
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98474...
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	aaggocagacgcagtggctcacgcctgtaatcccagcactttgggaggccgaggtgggc 13	3284
62 138285	<pre>gaatcacctgaggtcaggagttcgagaccagcctgaccaatatcgtgaaactccatctt 121 </pre>	1 3342
122 138343	actaaaaatacaaaaattagccaggtgtggtggcgggtgcttgtagtcccagctactt 179 	9 3392
180 138393	gggaggctgaggcaggtgaattacttgaacctgggaggtggaggttgcaatgagccaaga 239:	9 8452
240	ttgcaccactgcactccagtgacagagcgagactccatctcaaaaaaaaaa	3 3512
294	aaaaaagttgggaaaaggcca 314 	1 3572
315 138573	ggtgcagtggctccacgcctgtaatcccaacactttaagaggctgaggtgggagaatcct 374 	1 3631
375 138632	ttgagcccaggagttcgagaccagcctgggcattgtcccaagaccttgtcttacaaaa 434 	1 3691
435	attagccgggtgtgtggtggcatacgtctgtggtcccagctattcgggaggctg 486	5 3751
487	aggcagggagattgcttgagcctaggagtctagggctgtagtgagctgtgatcacgtcac 546	5 3811
547	tgtactctagcctgggcaacagagcaagactctgtctccaaaaaagaaaataaagttggg 606	5 8871
607 138872	aaaggctcactaacttcatcagatgagaacaaagacatgtttgaagtgtgaggccgaa 664 	4 8931
665	gcctggagaacgctatgcgcccaggaaatgcagggcagcagactcaagatgccagcgc 724 	4 8990
725	ctgttctggaggcccagatgggccctgcaatgcccactcaccctgccctcttgccc 784	4 9050
785 139051	cagacatcaccggccccatcatcctgcagacgtaccgcgccattgccgactacgagaaga 844	4 9110 [.]
845	cacgggggacgtggtggaggtcgtggagaagagcg 90 	4 9170
905	agagoggicagacotoccacottacgggotocottococtggitgotoaggaacocacago 964	4 9230
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102	ggecetaaatgteeteeceaactgtgggtegeettetetetettagtgtgeaeeetg 10	-

139351 aggggataaagaaattgtaaccatcacatgctgctggtgagaatataacatggtacaact 139410 ----gtttcaccatgt 139646 Db 139767 ttatatgatcacgcaatcccacttaggatatacctaagagaaatgaactttgaaaatgtg 139826 139887 atgaaataaatgttcagaataagcaaatctatagaagttggtctttgaggagaaaca--- 139943 -----aagaatgagca----tgaatggggaatgagaaagggtttattttgggggc 139989 gcaagtctgaatataccaaaaa-----ctattgaattgtgcatttttaaatt 140072 139459 ttgagacggagtettgetatgttgeecaggetggagtgeagtggegeaateteggettae 139518 Db 139990 aataaaaatgttctaaa-------------tggatttcgtgatgattgt 140025 bb 140133 cggetcactgcaacetctgcctcctgggttcaagcaattctcccacetcagcctcctga- 140191 tgc-agcetettgeeteetgggtteeageaatteteetgeeteageeteetgggtagetgg 139577 139578 gattacaggcgcacaccaccacctggctaatttttgtattttagtagacatggg--- 139634 gcttggggggccctggcaggttgtgatgcccttggtctggacagggaaccaggaggaggagg 1679 1680 cagacgactcgggagagtgggaggccagtggtgtctgtggatatgtggccaggttcagtg 1739 1740 ggaagetgaaggatgageagaeettaggetcaggaaggagggetgeetggaagtggggge 1799 1502 ctgtaggggtgtggggagaaagggggc--aggcagggctcagggatattgagtgactgcttt 1559 2039 tggtggctgtgggcatctgtgcatggcaggccggggcggggcatgtctgcgtcttctgtc 1141 1142 tggatgggtatgggaccgtctgttcattatgaagtgggctcagagctgtgattctgtgag 1201 1442 agtoctgacgagacggaagacoctgagcccaactatgcaggtgcccctgcctccgagg 1501 catgigigicatgcatgcatgigaccicatigiccagigigigaggigaaggigacatiticcaaa atcatcactgaccagaaagggaaaactggcagtgccagggctggatgggcctgcattga agggagccgctggggcctcagtcacattcccgcacctctggcacaggttggtgg tetgaggacattggacatcagtgtgtctgtgtcctgtgtcctcaccatccctgatggctgc 1560 ggagtctgggctggttgctggcttggcagaaaagtcagggctaagatctcatcggctctg cageteactgeaacetetgeeteccaggateaagtgattetecageeteageeteccag 1202 1322 1262 Db 139944 1860 1920 1082 139519 1800 140026 140073 1980 139635 Qy q Ωy a οy QQ q οy QQ δy qq δy ōλ QY g QΥ qq οy Qy ΟŊ qq ф Óγ ōλ δy QY οy

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10.011	exon intron exon
2160 gocteggcctcccaaagtgctggaattacagatgtgagcactgtcctggcctgg 1111	
$\overline{\mathbf{r}}$	gcctcggcctcccaaagtgctggaattacagtgtgagccactgtcctggcctg cccatttaaaatgggtgtgggttacaggggtgagccactggcctg cccatttaaaatgggtgattacagggttacagggtgagccactaggcctg cccatttaaaatgggtacatttatggtgtgtgaattgtgtctcaataaggctttt tttttttttt

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The invention relates to nucleic acids from human chromosome 2p21-16.3 and the encoded peptide (and mouse and chicken orthologues) that comprises a PGECCPLP group, an insulin-like growth factor binding protein (IGFBP)-11ke domain, cysteine-rich domains, an RGD (undefined) group and a transmembrane domain. The protein, e.g. CRIMI, interacts with peptides of the transforming growth factor superfamily. A composition comprising an expression construct comprising the nucleic acids of the invention or a mimetic which antagonises or mimics an activity of a CRIMI polypeptide may be used in a method for modulating the biological activity of a polypeptide of the bone morphogenic protein (BMP) family. In this way they may be used to prevent or treat an eye disease, contract formation. They may also be used to treat an eye disease, neurodegenerative diseases, renal and kidney disease, bone and tooth abnormalities, wounds and skin damage, e.g. by use of the nucleic acid in gene therapy by using antibodies directed against CRIMI polypeptides. The CRIMI gene.
                                                                                                                                                                                                                        Nucleic acids from human chromosome 2p21-16.3 and the encoded peptide, useful for preventing, diagnosing and treating e.g. eye disease, especially cataract formation -
                                                                                                                                              ï
                                                                                                                                            Wilkinson
                                                                                                                                            Kolle G,
                                                                                                                                            Georgas K,
                                                                                                                                          ڻ
ن
                                                                                                                                                                                                                                                                                                          Claim 4; Fig 3; 169pp; English
                                                                                                                                            Holmes
               24-NOV-2000; 2000WO-AU01435.
                                                          99AU-0004348
                                                                                                 (UYQU ) UNIV QUEENSLAND
                                                                                                                                          Yamada T,
                                                                                                                                                                                 WPI; 2001-343951/36.
                                                          26-NOV-1999;
                                                                                                                                          Little M,
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Sequence 236303 BP; 70199 A; 46544 C; 47996 G; 71563 T; 1 other;

ŝ DE 208281 CAGGGTCTTGCTGTATTGCCCAGGCTGGAGTGCAGTGCTGCCATCTGGGCCCACTGCAGC 208222 Db 208336 GCAGTGGTGCTTGAGATACTAAATTCTACCTGACA----TACATTCTTTTTTTTGAGA 208282 2170 Gaps 1940 ctcactcccttgctaaggctggagtgcggtggtgctatctcagctcactgcaacctctgc 208575 ATCCCCGGTTCCAGCGATTCTCCTCGCCTCAGCCTCCCGA-GTAGCTGGGATTACAAGTGT 2111 ccaggitiggccagactiggtctcgaactictgacctcaggitgatctgcctgcctcggcctc 2291 caaagtctggctctgtcacccaggctggagtgcagtaatgcaatctcagtcactgcaac 2000 ctcccaggatcaagtgattctccagcctcagcctcccaggtagctgggattacaagcat 208456 CCAIGTIGGCAGGCTIGTCTIGAACTCCTGATCTCAGGTGATCCACCTGCCCTGGACTC 208396 CCAAAGTGCTGGGATTACAGGAGTGAGCCACAGTGCCCACCGTTTTTCCCCTTTATCTAA ccaaagtgctggaattacagatgtgagccactgtccctggcctggttacccacattttaa 23; Length 236303; 150; Indels Score 363; DB 22; Pred. No. 4.4e-73; 0; Mismatches 10.8%; 75.3%; Conservative Query Match Best Local Similarity Matches 526; Conserv 1880 2171 qq g g qq ò qq g á ò δy ò Οy ò Ω

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Db 208221 CTCTACCTCCTGGGTTCAAGCGGTTCTCTGCCTCAGCCTCCTGAGTAGC--TGGGATGA 208164
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Search completed: January 11, 2002, 17:09:37 Job time: 28929 sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	5080 Homo s	0008 Homo	883 Homo	1166	1614 HOMC	371 Homo s	39 Homo	34 Ношо	13 Homo sapi	25 Homo	Papi	AC027219 Homo sapi	lomo s	01	Jomo s	Huma	Homo	Homo	Human	HOMO S	Human	Human	Human	Ношо		HOMO	Human	O MOE				J. HOMO	Homo	OHOHO O	5779 HOMO	0290 Homo	10 Human	1864 Homo s	310 Human C	352	1600 Homo sa	9634 Homo s	3461 Human D
QI	AC005080	909	AC004883	3176	191	7P43S0	\sim	7 PHOX 0	7P41S0	L14S0	AC092405	AC027219	HSNCF1S4	HS39NCF5	HS39NCF6	AC002477	AC027219	AL589985	HS694E4	AL591212	AL139396	HS268H5	AL139396	AC012482	AL354671	AL590226	HSJ469AI3	AC007666	AC008103	AC068198	AC026539	AC026333	AL590822	AC025990	AF196779	AC010290	HUAC002310	AC091864	HUAC002310	AC018521	AC020600 .	AC009634	HSDJ90108
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ALIGNMENTS .

		PRI 02-OCT-2000	Homo sapiens BAC clone CTA-269P13 from 7q11.2, complete sequence.	•					Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			Toward a complete human genome sequence	(1998)			Scott, K., Layman, D., Kalicki, J. and Harmon, G.	The sequence of Homo sapiens BAC clone CTA-269P13		
		DNA	CTA-26						rdata;	mates;		ton, R.	denom	7-1108			licki,	piens		
		dq 9	clone		770715				oa; Cho	ia; Pri	24526)	Waters	e human	1), 109		24526)	,D., Ka	Homo sa		
		12452	ens BAC		3 GI:7			sus	Metaz	Euther	1 to 1	E. and	complet	3.8 (1		1 to 1	Layman	ce of	ğ	
		AC005080 124526 bp	Homo sapie	AC005080	AC005080.2 GI:7770715	HTG.	human.	Homo sapiens	Eukaryota;	Mammalia;	1 (bases 1 to 124526)	Sulston, J.E. and Waterston, R.	Toward a	Genome Res. 8 (11), 1097-1108 (1998)	99063792	2 (bases 1 to 124526)	Scott, K.,	The sequer	Unpublished	
RESULT I	AC005080	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM			REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	REFERENCE	AUTHORS	TITLE	JOURNAL	

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COMMENT

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A1609282 (NID:94618449) tw83h06.x1"
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306. .652
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335. .520
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST AW204636 (NID:96504108)
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complement(106. .396)
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Location/Qualifiers
1. .124526
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1834, 1886
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    FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (02-OCT-2000) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On May 12, 2000 this sequence version replaced gi:3212911.
                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (12-JUN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                            Submitted (12-JUN-1998) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clone CTA-269P13 is from a release of the human BAC library CTB-HS-A. The library contains cloned DNA from human sperm. See: Shizuya et al., Proc. Natl. Acad. Sci. USA 89:8794-7 (1992); U-J. Kim et al., Genomics 34:213-8 (1996). The clone is available from Research Genetics, Inc. (http://www.resgen.com).
                                                                                                                                                                                                              Sequencing Center, Washington
4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTICE: This sequence may not represent the entire insert of this colone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mailto:egreen@nhgri.nih.gov , or see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
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                                                                                                                                                                                   ---- Genome Center
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Waterston, R.
  3 (bases 1 to 124526)
Waterston, R.H.
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                                              Direct Submission
                                                                                                                                                                                                                                                                                                        Waterston, R.H.
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The clone sequenced to the left is RP4-754G14; the clone sequenced to the right is RP11-396K3. Actual start of this clone is at base position 1 of CTA-269P13; actual end is at base position 124526 of

NEIGHBORING SEQUENCE INFORMATION:

The clone CTA-269P13 may contain a transposon in the growth of the clone, which is not part of the submitted sequence.

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6207. :6397
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ζς Qα	1800 117933	atcatcactgaccagaaagggaaaactggcagtgccagggctggatggggcctgcattga 1859
oy Op	1860	gcttgaaaaaactataatagaattggttaccattttattttattttattta
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D OY	2040	gtagotgggattacaagcatgcaccaccatgcctggataatttttgtattttagttgag 2099
Ολ Db	2100	acggggtttcaccaggttggccagactggtctcgaacttctgacctcaggtgatctgcct 2159
Oy Op	2160	gcctcggcctcccaaagtgctggaattacagatgtgagccactgtccctggcctggttac 2219
Oy Dp	2220 118353	ccacattttaaaatggagtgatttcacccttttatgtggatttacagcttgttttttt 2279
ολ	2280	tttttttgagacaaagtctggctctgtcacccaggctggagtgcagtaatgcaatctcag 2339
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γq	2400	cctggggttacaggcatgcaccaccacgccaggctaatttttgtatttttagtagagat 2459
γq	2460	ggggtttcgccatgttggccaggctggtctcgaactcctgacctcaggtgatccgccgc 2519
Qy Db	2520	cttggcctcccaaagtgctaggattacaggtgggaaccaccttgcccagcctgtggctat 2579
O D D	2580 118710	cgtttaaacactgggaaggcctgcagccccaggccgacagttagctgcagctgagcagt 2639
	2640	teceggtgceggtgagaeggatgetceaeceaectacteatggetgatetettgteatag 2699

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Db 119310 ACCCATCTGAGTCAGCCCCAGCAGGACGGGGTGTTTAGGGATCTGGGGTGACTGTCCC 119369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 23055).
Sulston, J.E. and Waterston, R.
Sulston, J.E. and Waterston, R.
Genome Res. 8 (11), 1097-1108 (1998)
                                                                             Db 119370 TGGGACTCTGGGTAAGCCACTGCCCCTCTCTGGGCTTAGTTTCCATCTCAGTAGCAGGA 119429
                                                                                                                                                                                                                                                  119190 CTACACTGCTGTGGAGGGGACGAGGTGTCTGCTGCTGCAGGGTGAAGCTGTTGAGGTAAT 119249
Db 118770 TCCCAGTGCCAGGTAGACGGATGCTCCACCCACCTACTCATGGCTGATCTCTTGTCATAG 118829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens BAC clone CTA-350L10 from 7q11.2, complete sequence. AC005098
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Threide,J., Abbott,A., Graves,T., Elliott,G. and M. The sequence of Homo saplens BAC clone CTA-350L10
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Waterston, R.H.
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COMMENT

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                                                                                                                                                                                                                                                                                                          Submitted (07-001-2000) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Jul 15, 2000 this sequence version replaced gi:3212893.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence CTA-350L10 from base position 222330 to 222775 is a GA rich region. The sequence is not exact but it is believed to be the best representation of this region. The region was sized by PCR from clone DNA at 650 bp. The region corresponds to restriction digest hindii: band size 7685 in silico and 7756 real.
                                                                                                                                                                 Submitted (15-JUL-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clone CTA-350L10 is from a release of the human BAC library CITB-HS-A. The library contains cloned DNA from human sperm. See: Shizuya et al., Proc. Natl. Acad. Sci. USA 89:8794-7 (1992); U-J. Kim et al., Genomics 34:213-8 (1996). The clone is available from NECTOR: pBeloBAC11
                                                    Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTICE: This sequence may not represent the entire insert of this colone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NEIGHBORING SEQUENCE INFORMATION:
Actual start of this clone is at base position 1 of CTA-350L10;
actual end is at base position 230552 of CTA-350L10.
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                        Sequencing Center, Washington 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                Center: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                    Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center project name: H_RG350L10
Direct Submission
Submitted (12-JUN-1998) Genome
University School of Medicine,
MO 63108, USA
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4 (bases 1 to 230552)
Waterston, R.H.
                                                                                                                                                                                                                 MO 63108, USA
5 (bases 1 to 230552)
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Direct Subm
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                                                                                                                                                Direct
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/organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="7"

/clone="CTA-350L10"

Location/Qualifiers

source

FEATURES

AI696334 (NID:94984234) tw59e05.x1" AA794004 (NID:g2856959) vr37a02.rl" EST A1700706 (NID:94988606) we39e12.x1" AW197058 (NID:96476288) xb15f09.x1" EST AI566941 (NID:94525393) tn25b07.x1" AW163398 (NID:g6302431) au94g04.yl" EST A1700706 (NID:94988606) we39e12.x1" AI566941 (NID:94525393) tn25b07.x1" AW197058 (NID:g6476288) xb15f09.x1" EST AW163398 (NID:g6302431) au94g04.y1" H70120 (NID:g1040326) ys01a09.rl" H72453 (NID:91044269) ys04f07.rl" N56845 (NID:91200735) yw83e04.rl" N56845 (NID:g1200735) yw83e04.rl" H89808 (NID:g1080238) yu82g03.r1" EST T79157 (NID:9697666) yd70b07.s1" EST R22057 (NID:9776838) yh25f08.s1" R22113 (NID:9776894) yh25f08.r1" AW383168 (NID:96887827)" AW503416 (NID:97139965)" AW993840 (NID:98254025)" BE000775 (NID:98261008)" AW523936 (NID:97166321)" AW503416 (NID:97139965)" AW523936 (NID:97166321)' EST AA078486 (NID:91837960)" EST T31784 (NID:q613882)" EST T30644 (NID:g612742)" EST T31784 (NID:9613882)" EST EST EST EST EST EST EST EST /rpt_family="Alu"
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Pred. No. 0;
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Best Local Similarity 99.4%;
Matches 3340; Conservative
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                                                       gttgggaaaggeteaettaaetteateagatgagaacaaagaeatgtttgaagtgtgagge
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Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
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Homo sapiens PAC clone RP4-771P4 from 7q11.21-q11.23, complete
sequence.
                                                                                                                                     2821 cccccagagtgggtgccagcaggagcttgccgagggatctgggatggaggagggtgg
                                                                            The sequence of Homo sapiens PAC clone RP4-771P4
Unpublished
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Mammalla; Euthoria; Primates;
1 (bases 1 to 13135)
Sulston,J.E. and Waterston,R.
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Kalicki, J. and Laplant, Y.
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AC004883.2 GI:4263746
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Waterston, R.H.
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/rpt0..6981
/note="similar to EST AI346557 (NID:94083763) gp46d02.xl"
7127..7471
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70cte="match to EST AI149529 (NID:g3677998) qc70f05.x1"

7567. .7859
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8604. .8708
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3424. .3947
//note="match to EST N39030 (NID:g1162237) yv22d08.s1"
3445. .3819
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2043. .2408
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                                                                                                                           /note="match to EST T82859 (NID:g711147) yd42b05.rl"
373. .854
                                                                 87. .549 '
/note="match to EST T90283 (NID:9718796) yd42c06.s1"
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'note="match to EST T06057 (NID:9317206)"
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8604. .8708
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6359. .6671
/rpt_family="Alu"
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1716. .4992
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/note="match to EST
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5005. .5265
/rpt_family="Alu"
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8381, .8683
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1111. .1407
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1649. .2063
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5522, 5800
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3052. .3361
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/gene="GTF2I"
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The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this Sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7, send mailto:egreen@nhgri.nih.gov , or see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This clone was derived from human PAC library RPCI-4, prepared by petere de Jong and coworkers at the Roswell Park Cancer Institute (http://pacpac.med.bufafalo.edu) using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994). The library is from
                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                       Washington
Missouri 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63108, USA
oubmitted (12-JUN-1998) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The clone may be obtained either from Genome Systems, Inc. (http://www.genomesystems.com) or Research Genetics, Inc. (http://www.genomesystems.com) or from Pieter de Jong. VECTOR: pryPAC2

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP5-1186P10. Actual start of this clone is at base position 1 of RP4-771P4; actual end is at 131359 of RP4-771P4.
                                                                                                                                              Direct Submission
Submitted (20-FEB-1999) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108,
5 (bases 1 to 131359)
Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence was finished as follows unless otherwise noted:
                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (21-DEC-1999) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 6:
On Feb 24, 1999 this sequence version replaced gi:3309099.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                              Direct Submission
Submitted (18-MAR-1999) Department of Genetics, I
University, 4444 Forest Park Avenue, St. Louis, I
6 (bases 1 to 131359)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   site: http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project name: H_DJ0771P04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens'/db_xref="taxon:9606"
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/clone_lib="RPCI-4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---- Genome Center
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                                                                                       4 (bases 1 to 131359)
Waterston, R.
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source

FEATURES

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EIEVTVEGPUNNNPOTSAVRPPTQTNGSNVPFKPRGREFSFEAMNAKITDLKOKVENL
FNEKCGEALGLKQAKKVPFALFESPEDFYVBGLPEGVPFRRPSTFGTPRLEKILRNK
KKFIIKRPEMFETAINESTSSKSPPRKINSSPNWITTASRSVEDLNIQVIPDDDN
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PVEDLVVEGLEDEGIPRRRPSYGIPRLERILLAKERIREVIKHELLUSTREDLÖLDK
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HHSSEGNEGTEMEVPAEDSTQHVPSETSEDPEVEVTIEDDDYSPPSKRPKANELPQPP
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GIPRLERIVRGSNKIKFVVKKPELVISYLPPGMASKINTKALQSPKRPRSPGSNSKVP
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                                                                            /product="general transcription
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8, USA
es 1 to 169604)
Submission
ed (23-MAY-2001) Genome Sequencing Center, Washington
ity School of Medicine, 4444 Forest Park Parkway, St. Louis,
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ed (04-OCT-2000) Genome Sequencing Center, Washington
ity School of Medicine, 4444 Forest Park Parkway, St. Louis,
8, USA
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                      tragccccagccaggacgggtgtttagggatctggggtgacttgtccct 3240
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/db_xref="taxon:9606"
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Submitted (01-JUL-2000) Department Of Chemistry And Biochemistry, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
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Ren,Q., Burian,D., Huang,E., Meadows,S., Korenberg,J. and Roe,B.A. Direct Submission
Submitted (20-JUL-2000) Department Of Chemistry And Biochemistry,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (21-FEB-1998) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
              20-JUL-2000 complete sequence.
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Ren,Q., Burian,D., Huang,E., Meadows,S., Korenberg,J. and Homo sapiens Chromosome 7 BAC Clone 239c10
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Jul 1, 2000 this sequence version replaced gi:8779478
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Clone 239c10,
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/db_xref="taxon:9606"
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Burian, D.M. and Roe, B.A.
Direct Submission
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oy Op	1081	9t99t9gct9t9ggcatctgtgcatggcaggccggggcgggg	1140
Oy Dp	1141	ctggatgggtatgggaccgttctttattatgaagtgggctcagagctgtgattctgtga 	1200
Qy Db	1201	gcatgtgtgcatgcatgtgacctcattgtccagtgtggtgaaggtgacatttccaa [1260
Oy Dp	1261	atctgagcattggacatcagtgtgtctgtgtgtcctgtgtcctcaccatccctgatggctg 	1320
Qy Dp	1321	caggagaccettggcccttcagtcacattcccgcactttggcacagttggtg	1380
δ _γ	1381	gttctgtcagatgaaagcaaagcgaggctggatcccagcatcttcctcgagcccctgga 	1440
Qy Dp	1441	cagtoctgacgagacggaagacctgagoccaactatgcaggtgcccctgcctccgag 	1500
Qy Dp	1501	gctgtaggggtgtgggagaaaggggcaggcatcagggatattgagtgactgctttg 	1560 45153
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Qy Db	1681 45274	agacgactcgggagagtgggaggccagtggtctgtggatatgtggccaggttcagtgg 	1740
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Qy Db	1801 45394	tcatcactgaccagaaagggaaaattggcagtgccagggctggatggggctgcattgag 	4
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Oy Dp	1921 45514	tactttttggggtatagagtctcactcccttgctaaggctggagtgcggtggtgctatctc 	1980 45573
Qy	1981	agctcactgcaacctctgcctcccaggatcaagtgattctccagcctcagcctcccagg	2040
Oy Dp	2041	tagctgggattacaagcatgcaccaccatgcctggataattttgtattttagttgaga 	2100
Qy	2101	cggggtttca-ccaggttggccagactggtctcgaacttctgacctcaggtgatctgcct 	2159 45753

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gcctcggcctcccaaagtgctggaattacagatgtgagccactgtccctggcctggttac
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Chanock, S.J., Roesler, J., Zhan, S., Hopkins, P., Lee, P.,
Barrett, D.T., Christensen, B.L., Curnutte, J.T. and Gorlach, A.
Genomic structure of the human p47-phox (NCF1) gene
Blood Cells Mol. Dis. 26 (1), 37-46 (2000)
Catarrhini; Hominidae; Homo
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Chancok, S.J., Roesler, J., Zhan, S.; Hopkins, P., Lee, P., Christensen, B.L., Curnutte, J.T. and Goerlach, A.
Direct Submission
Submitted (08-SEP-1999) Pediatric Oncology Branch, NCI, NIH/10/130240, Bethesda, MD 20892, USA
1. 17302
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Mismatches
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Homo sapiens p47-phox (NCF1) gene,
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/chromosome="7"
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Mammalia; Eutheria; Primates;
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/gene="NCF1"
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qq	11193		11252
Οy	1141	tggatgggtatgggaccgtctgttcattatgaagtgggctcagagctgtgattctgtg	1200
qq	11253	TGGGCTCAGAGCTGTGATTCT	11312
Qy	20	tgtgcatgcatgcatgtgacctcattgtccagtgtggaggtgaaggtgacatttccaa	260
QQ	11313	CATGTGTGCATGCATGCATGTGACCTCATTGTCCAGTGTGGAAGGTGACGTTTTCCAA .	11372
οy	26	alctgagcaltggacalcagtgtgtctgtgtccctgtgtcctcaccalcctgatggtg 1	320
qq	11373	TCTGAGCATTGGACATCAGTGTGTCTGTGTCCCTGTGTCCTCACCATCCCTGATGGCTG	11432
ογ	32.	cagggagccgctgggccctgcccctcagtcacattcccgcacctctggcacaggttggtg 1	
qq	11433	AGGGAGCCGCTGGCCCTGCCCTCAGTCACATTCCCGCACCTCTGGCACAGGTTGGTG	11492
Qy	1381	gttctgtcagatgaaagcaaagcgaggctggatcccagcatccttcct	1440
qq	11493	TTCTGTCAGATGAAAGCAAAGCGAGGCTGGATCCCAGCATCCTTCTCTCGAGCCCTTG	11552
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Qy	1561	gagtottgggttggttgctggcttggcagaaagtcagggctaagatotcatcggctctgg 1	1620
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Οÿ	1981	ageteactgeaacetetgeeteceaggateaagtgattetecageeteageeteceagg	2040
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QY	2041	acaagcatgcaccaccatgcctggataatttttgtattttagttgaga	2100
QC QC	12151	AGCTGGGATTACAAGCATGCACCACGATGCTGGATAATTTTTGTATTTTTAGTTGAG	12210
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Oy	2161	cctcggcctcccaaagtgctggaattacagatgtgagccactgtccctggcctggttacc 2	2220

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clone P43 is a p47-phox pseudogene presence of a GT deletion at the \,
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Gorlach, A., Lee, P.L., Roesler, J., Chanock, S.J. and Curnutte, J.T.
Direct Submission
Submitted (17-JUN-1996) Molecular and Experimental Medicine, The
Scripps Research Institute, 10550 N. Torrey Pines Rd., CAL 1, La
Jolla, CA 92037, USA
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3348)
Gorlach, A., Lee, P.L., Roesler, J., Hopkins, P.J., Christensen, B., Green, E.D., Chanock, S.J. and Curnutte, J.T.
A p47-phox pseudogene carries the most common mutation causing p47-phox deficient chronic granulomatous disease
J. Clin. Invest. 100 (8), 1907-1918 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 3348)
Chancock,S.J., Roesler,J., Hopkins,P.J., Lee,P.L., Bassett,D.T.,
Christensen,B., Curnutte,J.T. and Gorlach,A.
Genomic structure and the identification of multiple polymorphis
3301 ggatgagcccacccttgcctgtcttgtggggatccaatgtccttgtccaagtgggtgcat 3360
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Qy	1962 1679	agtgcggtggtgctatctcagctcactgcaacctctgcctcccaggatcaagtgattctc 2021
Qy	2022	cagcctcagcctccccaggtagctgggattacaagcatgcaccaccatgcctggataatt 20
Qy	2082	tttgtatttttagttgagacgggtttcaccaggttggccagactggtctcgaacttctg 2141
Qy	2142	acctcaggtgatctgcctgcctcggcctcccaaagtgctggaattacagatgtgagccac 2201
Qy	2202	tgtccctggcctggttacccacattttaaaatggagtgatttcacccttttatgtggatt 2261
Qy	2262	tacagcttgtttttttttttttttgagacaagtctggctctgtcaccaggctggagt 2321
Qy Db	2322	gcagtaatgcaatttcagctcactgcaaccttagcctcctgggttcaagcaattctcctg 2381
Qy	2382	cctcagccaccigagtagcctggggttacaggcatgcaccaccaccaggcagg
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clone P40 is a p47-phox pseudogene presence of a GT deletion at the
                                                                                                                                                          Unpublished

3 (bases 1 to 3350)

Gorlach, A. Lee, P.L., Roesler, J., Chanock, S.J. and Curnutte, J.T. Direct Submission
Submitted (19-JUN-1996) Molecular and Experimental Medicine, The Scripps Research Institute, 10550 N. Torrey Pines Rd., CAL 1, La Jolla, CA 92037, USA
1 (bases 1 to 3350)
Gorlach, A., Lee, P.L., Roesler, J., Hopkins, P.J., Christensen, B., Green, E.D., Chanock, S.J. and Curnutte, J.T.
A p47-phox pseudogene carries the most common mutation causing p47-phox- deficient chronic granulomatous disease
J. Clin. Invest. 100 (8), 1907-1918 (1997)
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Chancock,S.J., Roesler,J., Hopkins,P.J., Lee,P.L., Bassett,D.T.,
Christensen,B., Curnutte,J.T. and Gorlach,A.
Characterization of the genomic structure of the p47-phox gene
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/note="Human genomic P1 cl
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/gene="NCF1"
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/db_xref="taxon:9606"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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RESULT 8 HS47P40S02 LOCUS DEFINITION

ACCESSION KEYWORDS SEGMENT VERSION

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Submitted (09-MAY-1996) P. Lee, Molecular and Experimental
Medicine, Scripps Research Institute, 10550 North Torrey Pines
La Jolla, CA 92037, USA
Location/Qualifiers
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1 (bases 1 to 3349)
Gorlach, A., Lee, P.L., Roesler, J., Hopkins, P.J., Christensen, B., Green, E.D., Chanook, S.J. and Curntte, J.T.

A p47-phox pseudogene carries the most common mutation causing p47-phox deficient chronic granulomatous disease
J. Clin. Invest. 100 (8), 1907-1918 (1997)
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Chanock, S.J., Roesler, J., Hopkins, P., Lee, P., Bassett, D.T., Christensen, B., Curnutte, J.T. and Gorlach, A. Genomic Structure and the Identification of Multiple Polymc
2936 TCTGGGGTGACTTGTCCCTGGGACTCTGGGTAAGCCACTGCCCCTCTCTGGGCTTAGTTT
                                                                                     geoccaggetgggecegaceteacaetgtgetetetgtgeeettgeegtggaeeaggtgagee
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Gorlach,A., Roesler,J., Christensen,B., Chanock,S.J. and
Curnutte,J.T.
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exons 6-8.
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HOmo sapiens P47-phox (NCF1) gene,
U57834 GI:2754710
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Oy Db	1362	cctctggcacaggttggtgttctgtcagatgaaagcaaagcgaggctggatcccagcat 1421
Oy Dp	1422	cettectegagecetggaeagtectgaegagaeggaagecetgageceaactatgeag 1481
O D D	1482	gtgcccctgccctcgaggctgtaggggtgtgggaaaaggggcaggca
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Q.y D.b	1662	gggaaccaggaggaggagcagacgactcgggagagtgggaggccagtggtgtctgtggat 1721
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Oy Dp	2022 1738	cagcctcagcctcccaggtagctgggattacaagcatgcaccaccatgcctggataatt 2081
Qý Dp	79	tgtatttttagttgagacgggtttcaccaggttggccagactggtctcgaacttctg 21.
ογ	2142	acctcaggtgatctgcctcgcctcccaaagtgctggaattacagatgtgagccac 2201

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which is defined by the presence of a GT deletion at the
beginning of exon 2."
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Gorlach,A., Lee,P.L., Roesler,J., Christensen,B., Chanock,S.J. and
Curnutte,J.T.
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I bases 1 to 3200)
Gorlach,A., Lee,P.L., Roesler,J., Hopkins,P.J., Christensen,B., Green,B.D., Chanock,S.J. and Curnutte,J.T.
A p47-phox pseudogene carries the most common mutation causing p47-phox deficient chronic granulomatous disease
J. Clin. Invest. 100 (8), 1907-1918 (1997)
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Durect Submission
Submitted (19-JUN-1996) Molecular and Experimental Medicine, The
Scripps Research Institute, 10550 N. Torrey Pines Rd., CAL 1, La
Jolla, CA 92037, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                             Chanock, S.J., Roesler, J., Hopkins, P.J., Lee, P.L., Bassett, D.T., Christensen, B., Curnutte, J.T. and Gorlach, A.
Characterization of the genomic structure of the p47-phox gene
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KEYWORDS
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		ggagagtgggaggccagtggtgtctgtggatatgtggccaggttcagtgggaagctgaag 	GATGAGCAGCCTAGGCTCAGGAAGGAGGGCTGCCTGGAAGTGGGGGCATCATCACTGA CCAGAAAGGGAAAGGAGGCTGCCTGGAAGTGGGGGCATCATCACTGA CCAGAAAGGGAAAACTGGCAGTGCCAGGGCTGGATGGGGCCTGCATTGAGCTTGAAAAAA	actataatagaattggttaccattttattttatttattta	AGATAGAGTCTCACTCCTTGCTAAGGCTGGAGTGCGGTGGTGCTATCTCAGCTCACTGC aacctctgcctcccaggatcaagtgattctccagcctcagcctcccaggtagcttgggat ll	tacaagcatgcaccaccatgcctggataatttttgtattttagttgagacggggtttca 	ccaggttggccagactggtctcgaacttctgacctcaggtgatctgcctgc	ccaaagtgctggaattacagatgtgagccactgtccctggcctggttacccacattttaa 	aatggagtgatttcacccttttatgtggatttacagcttgtttttttt	caaagtctggctctgtcacccaggctggagtgcagtaatgcaatctcagctcactgcaac	cttagcctcctgggttcaagcaattctcctgcctcagccacctgagtagcctggggttac 	aggcatgcaccaccacgccaggctaatttttgtattttagtagagatgggtttcgcc 	atgttggccaggctggtctcgaactcctgacctcaggtgatccgccgccttggcctccc	aaagtgctaggattacaggtgggaaccaccttgcccagcctgtggctatcgtttaaacac 	tgggaaggeetgcaggeececaggeegttagetgcagetgageagtteecagtgeea 	ggtagacggatgctccacccacctactcatggctgatctcttgtcatagtgaagtgtctg

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Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Utheria; Primates; Catarrhini; Hominidae; Homo.
Lto 2899)
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rccacccaccractcargecrgarcrcrrgrcaragrgaagrcrcg 2276
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                            CCGTGGACCAGGTGAGCCATACGTCGCCATCAAGGCCTACACGCTG
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                                                                                                                   /note="Human genomic EMBL3A bacteriophage clone L14 is a p47-phox pseudogene which is defined by the presence of GT deletion at the beginning of exon 2" join(U1224.1:<879. .8119,1. .2866) /gene="NCF1"
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Direct Submission
Submitted (18-JUN-1996) Molecular and Experimental Medicine, T.
Scripps Research Institute, 10550 N. Torrey Pines Rd., CAL 1,
Jolla, CA 92037, USA
Location/Quallfiers
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                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
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Euteleostomi;
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1 (bases 1 to 18458)
Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.M.,
Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., Dietrich,N.L.,
Grantte,S., Guan,X., Gupta,J., Ho,S.-L., Idol,J.R., Karlins,E.,
Lee-Lin,S.-C., Mastrian,S.D., McCloskey,J.C., McDowell,J.,
Masiello,C., Mastrian,S.D., McCloskey,J.C., McDowell,J.,
Pearson,R., Prasad,A., Shevchenko,Y., Snyder,B., Stantripop,S.,
Thomas,J.W., Thomas,P.J., Touchman,J.W., Tsurgeon,C., Vogt,J.L.,
Walker,M.A., Wetherby,K.D., Zhang,L.-H. and Green,E.D.
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RP41-170F23, WORKING DRAFT
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelec
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence * as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319
Consensus quality: 179816 bases at least Q40
Consensus quality: 179898 bases at least Q20
Consensus quality: 181141 bases at least Q20
Insert size: 168000; agarose-fp
Insert size: 184058; sum-of-contigs
Quality coverage: 10.52x in Q20 bases; agarose-fp
Quality coverage: 9.60x in Q20 bases; sum-of-contigs
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7, USA
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Grovemont Circle, Galthersburg, MD 20877,
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Contact: nisc_mouse@nhgri.nih.gov
------ Project Information
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Papio cynocephalus anubis clone
SEQUENCE, 6 unordered pieces.
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Center clone name: 170F23
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                                                                                                                                                                                                                                                                                                                                                                        CCCCTCTCCATCCAGAGCACCCAT 2899
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13929 31257: contig of 17329 bp in length 31258 31357: gap of unknown length length 31358 42795: contig of 11438 bp in length 12796 42895: gap of unknown length 12896 61486: contig of 18591 bp in length 1478 61586: gap of unknown length 1587 111639: contig of 50053 bp in length 1640 111739: gap of unknown length 1640 111739: gap of unknown length 1640 111739: gap of unknown length 1740 184558: contig of 72819 bp in length 1740 18458: contig of 72819 bp in length 1740 18458: contig of 72819 bp in length 164858: contig of 72819 bp in length.
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/organism="Papio cynocephalus anubis"
/db_xref="taxon:9555"
/clone="RR41-170F23"
/clone_lib="RR41"
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/note="assembly_fragment"
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gactcaagatgccagcgcctgttctggaggcccagatgggccctgcaatgcccactcacc
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	1666 142806	accaggaggaggaggaggactcgggagagtgggaggccagtggtgtctgtggatatgt 1725
	1726 142746	ggccaggttcagtgggaagctgaaggatgagcagaccttaggctcaggaagga
, ,	1786 142686	ctggaagtgggggatcatcactgaccagaaagggaaaactggcagtgccagggctggat 1845
	1846 142626	ggggcctgcattgagct-tgaaaaaactataatagaattggttaccattttatttt
. 1	1904 142566	tattatttatttatttacttttttgagatagagtctcactcccttgctaaggc 1958
	1959 142506	tggagtgcggtggttatctcagctcactgcaacctctgc-ctcccaggatcaagtgat 2017
, , ,	2018	tetecagecteagectecccaggtagetggattacaageatgeaccaccatgeetggat 2077
,	2078 142387	aattitigtatititagtigagacggggtticaccaggtiggccagaciggtcicgaact 2137
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,-,	2198 142268	ccactgtccctggcctggttacccacattttaaaatggagtgatttcacccttttatgtg 2257
, -,	2258 142208	gatttacagcttgtttttttttttttttggacaaagtctggctctgtc-accca 2312
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, ,	2373	attctcctgcctcagccacctgagtagcctggggttacaggcatgcaccaccacgccagg 2432
,1	2433	ctaatttttgtatttttagtagagatgggtttcgccatgttggccaggctggtctcga 2492
•	2493 141970	actcctgacctcaggtgatccgccttggcctcccaaagtgctaggattacaggtgg 2552
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1	2613 141850	gccgacagttagctgcagctgagcagttcccagtgccaggtagacggatgctccacccac

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AC027219 149830 bp DNA HTG 03-MAR-2001
HOMO sapiens clone RP11-729P19, *** SEQUENCING IN PROGRESS ***, 79
uordered pieces.
AC027219
AC027219 3 GI:13184220
HTG; HTGS_PHASEI.
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Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F., Boushayiy,L., Boukhgalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Dlaz,J.S., Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Unpublished
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LOCUS
DEFINITION
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AUTHORS
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90: gap of 100 bp 134434: contig of 644 bp in length 43576: contig of 1242 bp in length 76: gap of 100 bp
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contig of 1648 bp in length
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62781: contig of 2126 bp in length
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69279: contig of 1512 bp in length
                                                                                                                             p of 100 bp contig of 1088 bp in length
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33690: contig of 1365 bp in length
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67667: contig of 1964 bp in length
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                                                                                                                                                                              21170: gap of 100 bp 22152: contig of 982 bp in length
                        p of 100 bp contig of 966 bp in length
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             Grand-Pierre, N., Grant, G., Hagos, B., Heatord, A., Horton, L., Howland, J.C., Illev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lagoque, K., Lamazares, R., Janders, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meholt, L., Mihova, T., Miranda, C., Menga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., O'Nell, D., Ollvar, T.M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Trajilio, J., Vasiliev, H., Viel, R., Vo, A., Milson, B., Wu, X., Wyman, D., Ye, W.J., Voung, G., Zainoun, J., Zimmer, A. and Zody, M., Travers, M., Trigillo, J., Vasiliev, H., Viel, R., Vo, A., Milson, B., Wu, X., Wyman, D., Ye, W.J., Voung, G., Zainoun, J., Zimmer, A. and Zody, M., Shallev, H., Viel, R., Vo, A., Milson, B., Wu, X., Wyman, D., Ye, W.J., Voung, G., Zainoun, J., Zimmer, A. and Zody, M., Shallev, H., Viel, R., Vo, A., Milson, B., Wu, X., Wyman, D., Ye, W.J., Non Mar 2, Zoll this sequence version replaced gi:11610941.

All repeats were identified using RepeatMasker:
Smit, A.F. A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/Repeatmasker.html
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  Graham, L.
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-------- Project Information
Center project name: L8346
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62: gap of 100 bp
6423: contig of 561 bp in length
23: gap of 100 bp
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Ginde, S.,
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Gorlach, A., Lee, P.L., Roesler, J., Christensen, B., Chanock, S.J. and
Curnutte, J.T.
                                                                                                                                                                                                                              HSNCFIS4 918 bp DNA PRI 07-JAN-1998
Homo sapiens p47-phox (NCFL) pseudogene, clone P38, exons 6 and 7.
U69642
                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 918)
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                       49855 GGGAACCACCTTGCCCAGCCTGTGGCTATCGTTTAAACACTGGGAAGGCCTGCAGCCCCC 49796
                                               2 (bases 1 to 918)
Chanock, S.J., Roesler, J., Hopkins, P.J., Lee, P.L., Bassett, D.T.,
Christensen, B., Curnutte, J.T. and Goriach, A.
Characterization of the genomic structure of the p47-phox gene
Unpublished
                                                                                                   acctactcatggctgatctcttgtcatagtgaagtgtctggacagaccttcatcgttatg 2730
gggaaccaccttgcccagcctgtggctatcgtttaaacactgggaaggcctgcagcccc 2610
                                                                                                                                                                           Gorlach, A., Lee, P. L., Roesler, J., Hopkins, P. J., Christensen, B., Green, E. D., Chanock, S. J. and Curnutte, J. T.
A p47-phox pseudogene carries the most common mutation causing p47-phox deficient chronic granulomatous disease
J. C. Lin. Invest. 100 (8), 1907-1918 (1997)
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Submitted (06-SEP-1996) Molecular
Scripps Research Institute, 10550
Jolla, CA 92037, USA
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/db_xref="taxon:9606"
/chromosome="7"
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Homo sapiens p.47-phox (NCF1) pseudogene, clone P39, exons 6 and U72360
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             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 904)
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                                                                                                                                              2 (bases 1 to 904)
Chanock, S.J., Roesler, J., Hopkins, P.J., Lee, P.L., Bassett, D.T.,
Christensen, B., Curnutte, J.T. and Gorlach, A.
Characterization of the genomic structure of the p47-phox gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aagcccctyccaaggctcaggcagcctggccctgggaggacgccagctctgttagggg 1027
                                                       Gorlach, A., Lee, P.L., Roesler, J., Hopkins, P.J., Christensen, B., Green, E.D., Chanock, S.J. and Curnutte, J.T.
A p47-phox pseudogene carries the most common mutation causing p47-phox- deficient chronic granulomatous disease
J. Clin. Invest. 100 (8), 1907-1918 (1997)
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Submitted (24-SEP-1996) Molecular and Experimental Medicine,
Scripps Research Institute, 10550 N. Torrey Pines Rd., CALI,
Jolla, CA 92037
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Pred. No. 8.1e-213;
0; Mismatches 7;
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Gorlach, A., Lee, P.L., Chanock, S.J. and
                                                                                                                                                                                                                                                                                                                             1. 904
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/db_xref="taxon:9606"
/chromosome="7"
/map="7q11.23"
/clone="P39"
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/gene="NCF1"
/number=7
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99.0%;
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Matches 897; Conservative
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Homo sapi 602300336

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AV762129 AV760497

AV764490 AO739838 AO543763 AV762129 AV760497 AO479821 BG386803 BF346320 BE796439

3081_B

Homo sapi EST388119

AV714931

AV700988 TBI-E1

AQ839831 260 AQ748222 HS. AQ878530 HS. AQ393450 CIT AV700988 AV7 BC009270 Hom AW976010 EST AV744931 AV7 AC74441 602

DKFZp434A

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Homosaplens Saplens Eutheria; Hominidae; Homo.

E. (Lobassa Lto 774)

National Institutes of Health, Mammalian Gene Collection (MGC)

(Inpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapDs-remail.inh.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

Contact: Robert Strausberg, Ph.D.

Colone distribution: Lich Home distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

Plate: LLCMGCS row; g column: 14

High quality sequence stop: 773.

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

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602638552F1 NIH_MGC_48 Homo sapiens CDNA clone IMAGE:4766245 5',
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Copyright (c) 1993 - 2000 Compugen Ltd.
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HS_3100_A Homo sapi CITBI-E1-CITBI-E1-

ALS27073 AQ890095 BC007465 AQ393450 AQ356404 BF900703 BG260565

673.2 335.2 335.2 334.2 334.0 334.0 334.0 334.0 334.0 334.0 336.8

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/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI; Site_2: ECORI; CDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MCC Library."
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Pred. No. 3.5e-65;
0; Mismatches 8; Indels
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                                                                                                                                                                 Query Match 20.0%;
Best Local Similarity 98.8%;
Matches 678; Conservative (
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3 31-MAR-2000 260L13, DNA sequence.

AQ839852 15970 bp DNA GSS 260L13-C56 CITB Homo sapiens genomic clone AQ839852 GI:6652484 GSS.

LOCUS

ACCESSION VERSION

KEYWORDS

AQ839852/c

RESULT

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9
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (Daess I to 15970)
Carpten, J.D., Makalowska, I., Robbins, C.M., Scott, N., Sood, R., Connors, T.D., Bonner, T.I., Smith, J.R., Faruque, M.U., Stephan, D.A., Pinkett, H., Morgenbesser, S.D., Su, K., Graham, C., Gregory, S.G., Williams, H., McDonald, L., Baxevanis, A.D., Klingler, K.W. and Landes G.M.
                                                                                                                                                    A.6-Mb high-resolution physical and transcription map encompassing the hereditary prostate cancer 1 (HPC1) region Genomics 64 (1), 1-14 (2000) 20179426
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Pred. No. 5e-32;
0; Mismatches 145;
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                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
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/clone="260L13"
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Tel: 301 435 5626
Fax: 301 435 5465
Email: jdc@nhgri.nih.gov
                                                                                                                                                                                                                                             Cancer Genetics Branch
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77.2%;
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Matches 516; Conservative
                                                                                                                                                                                                                             Contact: Carpten
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Homo sapiens
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                                                                   AUTHORS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo.
1 (bases 1 to 743)
                                                                                                                                                                                                                                                                                     Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawal,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
                                                                                                                                                                                                                                                                                                                                                                     1081 gtggtggctgtgggcatctgtgcatggcaggccggggcggggcatgtctgcgtgttctgt 1140
                                                                                                                                             295 AGCGAGAGCGGTCAGACCTCCCACCTTACGGGGCTCCTTCCCGTGGTGCTCAGGAACCCA 236
    415 GCGACAGACATCACCGGCCCCATCATCCTGCAGACGTACCGCGCCATTGCCAATTACGAG 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AU130725 743 bp mRNA EST 24-OCT-2000 AU130725 NT2RP3 Homo sapiens cDNA clone NT2RP3001331 5', mRNA sequence.
                                          cagecacaagececetgecaaggeteaggeageetggeecetgggaggaeteetg
                                                                                                                                                                                                                                                                                                             agogagagaggtcagacotcccaccttacggggctccttcccctggtgctcaggaaccca
                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AU130725
AU130725.1 GI:10991079
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 459)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Halia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtmi2.pl?tl=CM2&t2=CM2-MT0190-091200-595-h10&t1=2000-12-09&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 12
High quality sequence stop: 458.
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                                                                                                                                                                                                                                                                                                      BF901739 459 bp mRNA EST 18-JAN-2001
CM2-MT0190-091200-595-h10 MT0190 Homo sapiens CDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shotgun sequencing of the human transcriptome with ORF expressed
                                                                           2444 tatttttagtagagatggggtttcgccatgttggccaggctggtctcgaactcctgacct 2503
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20202663
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Pred. No. 2.6e-30;
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/db_xref="taxon:9606"
/clone_lib="MT0190"
/dev_stage="Adult"
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139 c 136 q
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/note="Vector: pME18SFL3; mRNA from NT2 neuronal precursor cells after 2-weeks retinoic acid (RA) induction" 170 c 192 q 162 t 4 others
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'ف
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
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Pred. No. 6.8e-30;
); Mismatches 152;
                                                                                                                                                                                                                                         /cell_type="teratocarcinoma"/cell_line="NT2"
                                                                                                                                                     /organism="Homo sapiens"
                                                                                                                                                                          /db_xref="taxon:9606"
/clone="NT2RP3001331"
/clone_lib="NT2RP3"
                                                                                                          Location/Qualifiers
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75.98;
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Best Local Similarity 75.9
Matches 508; Conservative
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781 gcccagacatcaccggcccatcatcctgcagacgtaccgcgccattgccgactacgag 840

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 828)

Li.W.B., Gruber.C., Jessee.J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished (2001)

Contact: Genoscope
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                                                                               acctcaggtgatctgcctgcctcggcctcccaaagtgctggaattacagatgtgagccac
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                                                                                                                                                                                                                                                                                                         attatttatttattttattttacttttttgagatagagtctcactcccttgctaaggctgg
           455 ACCTCAGGTGATCCAACCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGTGTGTGAGCCAC
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                                         agtgcggtggtgctatctcagctcactgcaacctctgcctcccaggatcaagtgattctc
                                                                                                                           tttgtatttttagttgagacggggtttcaccaggttggccagactggtctcgaacttctg
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BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www
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Anote—"Organ: Drain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end centiched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Perhologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL: 192 c 199 g 193 t.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 348.8; DB 10; Length
Pred. No. 9.1e-30;
0; Mismatches 157; Indels
                                                                                             /tissue_type="neuroblastoma cells"
/lab_host="DH10B"
          /clone_icsObc017Y020"
/clone_lib="LTI_NFL003_NBC3"
/sex="male"
/db_xref="taxon:9606"
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75.2%;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                        Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
                                                                                                                                                                                 1 (bases 1 to 732)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="CIT Approved Human Genomic Sperm Library D"
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                           AQ890095 732 bp DNA GSS 10-NOV-1999 HS.3100.Al_E11_T7C CIT Approved Human Genomic Sperm Library D sapiens genomic clone Plate=3100 Col=21 Row=I, DNA sequence. AQ890095.1 GI:6346285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23;
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/clone="Plate=3100 Col=21 Row=1"
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 16 Row: k Column: 21 This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not
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Mammalia; Butheria; Primates; Catarrhin1; Hominidae; Homo.
1 (bases 1 to 1501)
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DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 943
Meb Site: http://www.shgc.stanford.edu
Contact: (Dickson, Mark) mcdepail.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (01-MAY-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                     tttttttttttttttgagacaaagtctggctctgtcacccaggctggagtgcagtaatg 2330
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This clone has the following problem: frame shifted
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/clone_lib="NIH_MGC_58"
/lab_host="DH10B"
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Contact: MGC help desk
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BC007465
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Tissue Procurement: ATCC
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Use of BAC End Sequences from CalTech Libraries for Sequence-Ready
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Homo sapiens genomic clone 2546H6, DNA
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
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              Contact: Shaying Zhao, William Nierman, Department of Eukaryotic Genomics
The Institute for Genomic Research
712 Medical Center Dr., Rockville, MD 21
Tel: 301 838 0200
Fax: 301 838 0208
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/db_xref="taxon:9606"
/clone="2546H6"
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Matches 503; Conservative
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Use of BAC End Sequences from CalTech Libraries for Sequence-Ready
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                                                                                                                                                                                                                                                                                                                                                            Unpublished (1997)
Other_GSSs: CTTBI-E1-2541D19.TR
Contact: Shaying Zhao, William Nierman, Mark Adams
Contact: Shaying Zhao, William Nierman, Mark Adams
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
The Institute for Genomic Research
The Institute for Genomic Research
The Institute for Genomic Research Genetics (info@resgen.com). BAC Enails hobetigr.org
Clones are available from Research Genetics (info@resgen.com). BAC end search page:
                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 680)
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Seg primer: M13-21
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CITBI-E1-2541D19.TF CITBI-E1 Homo sapiens genomic
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/note="Vector: pBeloBAC11;
CalTech Human BAC Library D
155 c 172 g 134 t
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/db_xref="taxon:9606"
/clone="2541D19"
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/sex="male"
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1 (bases 1 to 372)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveire, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., 'Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CMZ&t2=CM2-MT0190-071200-594-d03&t3=2000-12-07&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 34
High quality sequence start: 34
Liocation/Qualifiers
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CM2-WT0190-071200-594-d03 MT0190 Homo sapiens cDNA, mRNA sequence.
BF900703
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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Fax: +55-11-2707001
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SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
/716 - Ludwig Institute for Cancer Research) profiles
/116 - the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
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NIH-MGC http://mgc.ncl.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
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602372119F1 NIH_MGC_93 Homo sapiens CDNA clone IMAGE:4480109 9
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information car
flound through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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0; Mismatches 1; Indels 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                    stringency conditions."
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/organism="Homo sapiens"

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/clone_lib="NIH_MGC_93"
/clone_lib="NIH_MGC_93"
/fissue_type="transitional cell papilloma, cell line"
/lab_host="nH10B (phage-resistant)"
/note="Organ: bladder; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ctcagcctccccaggtagctgggattacaagcatgcaccaccatgcctggataattttg 2085
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Human Male BAC Library Homo sapiens
ol=17 Row=E, DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              456 TATITITAGTAGAGGGGGTTICACCATGTTGGCCAGGCTGGTCTCGAACTCCCGACCT 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     635 TITGITGITITITITITICITITICGAGAIGAGITITICCTCTTGTCGCCAGGCTGGAGTGC 576
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         575 AATGGGGGAATCTCGGCTCACTCGAACCTCCTGGGTTTCAAGCAATTCTCCTGC
                                                                                                                                                                                                                                                                                                                                                           10.0%; Score 336.8; DB 11; Length 948; 74.8%; Pred. No. 1.7e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches 122;
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HS_5505_A1_C09_T7A RPC1-11 Human
genomic clone Plate=1081 Col=17
AQ739838
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947 bp
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635 AACAAAACAA 644
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ORIGIN
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4
                                                                                                                                                                                                                                                                                                                 Email: jwallacego, washington.edu

Clones are derived from the human BAC library RPCI-11. For BAC

Clones are derived from the human BAC library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu.). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)

or from Resear h Genetics (info@resgen.com). BAC end Web Server:

http://www.htsc.washington.edu

Plate: 1081 row: E column: 17
                                                                Euteleostomi;
                                                                                                         Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  aaaaatacaaaaattagccaggtgtggtggcgggtgcttgtagtcccagctacttgggag 184
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                          scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 13; Length 877;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="Plate=1081 Col=17 Row=E" /clone_lib="RPCI-11 Human Male BAC Library"
                                                                                                                                                                                                                      Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
121: (206) 616-3818
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 335.6; DB 13; Length
Pred. No. 2.4e-28;
0; Mismatches 119; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 877.
Location/Qualifiers
 GI:5517360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tch 10.0%;
al Similarity 76.9%;
469; Conservative (
                                                                                               (bases 1 to 877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . .877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Class: BAC ends
40739838.1
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                                                                                                                                            Hood, L.
                                human.
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                                              ORGANISM
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                                                                                             REFERENCE
                                                                                                            AUTHORS
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="TMAGE:4753762"
/clone="TMAGE:4753762"
/clone="tmAGE:4753762"
/clone="type="squamous cell carcinoma"
/tissue_type="squamous cell carcinoma"
/lab_host="DH10B (Tl phage-resistant)"
/note="Organ: skin; Vector: pcWv-SPORT6; Site_1: NotI:
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
76 a 203 c 260 g 208 t
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1 (Dases 1 to 947)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-rémail.nih.gov
Tissue Procurement: James Cleaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov. o column: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                         -----TTACTGGTTGGGTGCGGTGGCT-CACGCTTATAATCCCAGCACTTTGGGAGGCC 394
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Pred. No. 5.4e-28;
0; Mismatches 143; Indels 13;
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Location/Qualifiers
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ilarity 74.7%;
Conservative (
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us-09-820-005-3_copy_10200_13560.rst

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 746)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs.r@mail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can
                                                            TTAAAAAAATAGCCAGGCAT----GGACATGGTAGTGCATACCTGTGGTCCCAGCCACT
                                                                                                  aggetgaggcaggtgaattacttgaacctgggaggtggaggttgcaatgagccaagattg
                                                                                                                                                   aaagttgggaaaaggccaggtgcagtggctccacgcctgtaatcccaacactttaagagg
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Plate: LLCM1207 row: c column: 09
High quality sequence stop: 728.
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/clone="InAGE:4335680"
/clone="In="NIH_MGC_48"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="NHH_MGC_48"
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/note="Organ: B-cells: Vector: pOTBY; Site_1: XhoI;
Site_2: Ecorl: cDNA made by oligo-dT priming.
Site_2: Ecorl: cDNA made by oligo-dT priming.
Directionally cloned into Ecorl/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 710)

S Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.

Homo sapiens genomic DNA, chromosome 21q

L Published only in DataBase (1998) In press

E 2 (bases 1 to 710)

S Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.

B Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.

S Matted (08-UUL-1998) to the DDBJ/EWBL/GenBank databases.

Masahira Hattori, Kitasato University, Department of Science, JST Sequencing Laboratory; Kitasato 1-15-1, Saqamihara 228, Japan (E-mail:hattori@hygc.ims.u-tokyo.ac.jp, Tel:0427-78-9561)
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 sapiens genomic DNA, 21q region, clone: 130N6SpN26, genomic
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0; Mismatches 161; Indels
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Best Local Similarity 73.73
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AG010073 AG003884
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Db 147 TTGGTATTTTAGTAGACGGGGTTTCACCATGTTAGCAGAGGTCTCAATTGCTGG 88
Oy 2500 acctcaggtgatccgccttggctcccaaagtgctaggattacaggtggaacca 2559
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Oy 2560 c 2560
Db 29 C 29
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(without alignments)
2698.403 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Gapop 10.0 , Gapext 1.0
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Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Seguence	Sequence	Sednence	Sequence	Seguence	Sequence
SUMMAKIES	ID	US-08-975-080-35	US-09-630-706-10	US-08-323-443B-1	US-08-658-136-2	US-08-658-136-1	US-08-814-095-7	PCT-US93-06251-81	PCT-US93-06251-80	US-08-257-963B-9	PCT-US95-07201-9	US-09-009-913-1	PCT-US95-07201-43	US-08-480-449-1	US-08-660-542-1	US-09-232-878-5	US-09-078-294-7	US-09-085-199B-44	US-08-687-080-101	US-09-009-913-1	US-08-814-095-7	US-08-687-080-101	US-08-273-411-2	-914-	-393-2	US-08-525-058A-5	-08-696-7	US-09-042-531-5
	DB	4	•	Н		٣	m	Ŋ	Ŋ	7	S	٣	Ŋ	-	7	4	4	4	7	٣	m	7	_	7	Н	٦	7	4
	Length DB	14796	14796	31571	53526	53577	ß	841	841	4421	4421	72928	22481	2923	2923	2927	11811	3715	5543	72928	35060	5543	3373	8174	8174	8174	8174	8174
æ	Query Match	10.1	10.1	10.0	10.0	10.0	9.8	9.8	9.8	9.7	7.6	9.6	9.6	9.5	9.2	9.5	9.5	9.4	9.4	9.4	9.3	9.3	9.3	9.3	6.9	9.3	9.3	9.3
	Score	339.2	339.2	335.4	335.4	335.4	330	329.6	328	326.6	326.6	321.8	321	318.6	318.6	318.6	318.6	317.2	316.4	316	314.2	313.6	312.6	312.6	312.6	312.6	312.6	312.6
	Result No.	-	7	٣	4	S	9 ပ	c 2		6	10	11	12	13	14	15	c 16	c 17	18	c 19	20	c 21	22	23	24	25	56	27

Sequence 3, Appli Sequence 6, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 6, Appli Sequence 1, Appli Sequence 1, Appli Sequence 22, Appli Sequence 22, Appli Sequence 22, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 10, Appli Sequence 10, Appli Sequence 20, Appli
PCT-US91-00899-3 US-09-173-914-6 US-09-173-914-6 US-09-197-636-3 US-07-197-636-3 US-07-197-636-3 US-07-841-652-1 US-08-09-173-914-6 US-08-058-136-2 US-08-058-136-2 US-08-058-136-2 US-08-058-136-2 US-08-05-07201-9 US-08-075-0039-07201-9 US-08-075-008-35 US-08-075-008-35 US-08-075-008-35 US-08-075-008-35 US-08-075-008-35 US-08-075-008-35 US-08-075-008-35 US-08-075-008-35 US-08-075-008-35 US-08-09-05-008-35
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ALIGNMENTS

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Length 14796;
                                                                      GENERAL INFORMATION:
APPLICANT: Altieri, Dario C.
TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
TITLE OF INVENTION: CELLULAR APOPTOSIS, AND ITS MODULATION
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE STATEM.

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/975,080

FILING DATE: 20-NOV-1997

PRIOR APPLICATION NUMBER: US 60/031,435

FILING DATE: 20-NOV-1996

APPLICATION NUMBER: US 60/031,435

FILING DATE: 20-NOV-1996

ATTORNEY-AGENT INFORMATION:

NAME: Adler, Reid G.

REFERENCE/DOCKET NUMBER: 044574-5022-01-WO

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECHONE: 202-467-7000

TELECHONE: 202-467-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 10.1%; Score 339.2; DB 4; Best Local Similarity 72.5%; Pred. No. 1.4e-71; Matches 557; Conservative 0; Mismatches 158;
                                                                                                                                                                                                                                               ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDUIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                            ; Sequence 35, Application US/08975080
; Patent No. 6245523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear ; MOLECULE TYPE: DNA (genomic) US-08-975-080-35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 14796 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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US-08-975-080-35
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Patent No. 6277640
GENERAL INFORMATION:
GENERAL THORMATION:
TITLE OF INVENTION: APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF HER
FILE REFERENCE: RTS-0053
CURRENT APPLICATION NUMBER: US/09/630,706
CURRENT APPLICATION NUMBER: US/09/630,706
NUMBER OF SEQ ID NOS: 94
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
LOCATION: (2811)...(2921)
NAME/KEY: CDS
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                                                                                         Indels
                                                                  Score 339.2; DB 4;
Pred. No. 1.4e-71;
0; Mismatches 158;
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Sequence 1, Application US/08323443B
Patent No. 5654170
GENERAL INFORMATION:
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                                                                   10.1%;
72.5%;
                     ; LOCATION: (11955)...(12044)
US-09-630-706-10
                                                                   Query Match 10.1
Best Local Similarity 72.5
Matches 557; Conservative
(5158)...(5275)
CDS
 LOCATION:
NAME/KEY:
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                                                                    2312 aggotggagtgcagtaatgcaatctcagctcactgcaaccttagcctcctgggttcaagc 2371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 335.4; DB 3;
Pred. No. 1.9e-70;
0; Mismatches 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patentin Release #1.0, Version #1.25
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APPLICATION NUMBER: US/08/658,136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-658-136-2; Sequence 2, Application US/08658136; Patent No. 6071717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6367 TGAGCCAACGCGCCCAGAC 6385
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; MOLECULE TYPE: DNA (genomic)
US-08-658-136-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 75.7%;
Matches 514; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ONE MOUNTAIN ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 508-872-5415 INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 53526 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENZYME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: FRAMINGHAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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                       APPLICANT: QIAN, FENG
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/323,443B
FILING DATE: 12-OCT-1994
CLASSIFICATION: 435
                                                                                                     ....nrESSEE: Darby & Darby PC STREET: 805 Third Avenue CITY: New York STATE: NY STATE: NSA STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Ludwig, S. Peter
REGIZTRATION NUMBER: 25,351
REFERENCE/DOCKET NUMBER: 0372,
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEPAS: (212) 753-6237
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC competible
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HYPOTHETICAL: NO
APPLICANT: GERMINO, GREGORY APPLICANT: QIAN, FENG
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TYPE: nucleic acid
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; CLONE: PKD1 GENOMIC
US-08-323-443B-1
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                          6734 TCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGAGACGGAGTCTTGCTCTTGTCTCCAGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: KLINGER, KATHERINE W
APPLICANT: LANDES, GREGORY M
APPLICANT: BURN, TIMOTHY C
APPLICANT: CONNORS, TIMOTHY D
APPLICANT: DACKOWSKI, WILLIAM
APPLICANT: GERMINO, GREGORY
APPLICANT: QIAN, FENG
TITLE OF INVENTION: POLYCYSTIC K
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Patent No. 6071717
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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STATE: MASSACHUSETTS
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                  Version #1.25
                                                                                                                                                                                                                                                                                                                                                   DB 3;
                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches 116;
                                                                                                                                                                                                                                                                                                                                                   Score 335.4; DB 3
Pred. No. 1.9e-70;
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                            APPLICATION NUMBER: US/08/658,136 FILING DATE:
                                                                                                                         31,845
R: GEN4-17.
                                                                                                                                                                                                             ; SEQUENCE CHARACTERISTICS:
; LENGTH: 5377 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-658-136-1
                                                                                                                     REGISTRATION NUMBER: 31,845
REFERENCE/DOCKET NUMBER: GE
TELECOMNUNICATION INFORMATION
TELEPHONE: 508-872-8400
TELEFAX: S08-872-5415
                                                                                                                                                                                                                                                                                                                                                   10.0%;
                                                                                                                                                                                   TELEFAX: 508-872-5415 INFORMATION FOR SEQ ID NO: 1:
                                                                             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LASSEN, ELIZABETH
                                                                                                                                                                                                                                                                                                                                                                                 Matches 514; Conservative
                                                                                                                                                                                                                                                                                                                                                                    Similarity
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2552 ggaaccaccttgcccagcc 2570

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us-09-820-005-3_copy_10200_13560.rni

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NAME/KEY: exon
LOCATION: complement (34528..34895)
LOCATION: complement (74528..34895)
OTHER INFORMATION: /function= "arsenite resistance
OTHER INFORMATION: /fene= "AR"
OTHER INFORMATION: /fene= "AR"
FEATURE:
NAME/KEY: exon
LOCATION: 2524.26009
LOCATION: 2524.26009
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /gene="AGHE"
OTHER INFORMATION: /fonmber= 3
FEATURE:
NAME/KEY: exon
LOCATION: 27005..27274
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /gene="ACHE"
OTHER INFORMATION: /number= 4
FEATURE:
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LOCATION: 27255..28007
LOCATION: A7255..28007
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /gene= "ACHE"
OTHER INFORMATION: /gene= "ACHE"
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 28008..28129
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /evidence-EXPERIMENTAL
OTHER INFORMATION: /gene-"ACHE"
OTHER INFORMATION: /number-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: exon
LOCATION: complement (32959..33094)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 6
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LOCATION: complement (34092..34358)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 2
FEATURE:
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LOCATION: complement (33493..33591)
OCHER INFORMATION: /gene="AR"
OTHER INFORMATION: /number= 4
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 7
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LOCATION: complement (33779..33963)
OCHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 3
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LOCATION: complement (33297..33408)
OCHER INFORMATION: /gene="AR"
OTHER INFORMATION: /number= 5
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27385..27387
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NAME/KEY: terminator
LOCATION: 28129..28131
FEATURE:
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LOCATION:
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LOCATION:
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                                                       RESULT 6
US-08-814-095-7/C
Sequence 7, Application US/08814095
Patent No. 6025183
GENERAL INFORMATION:
APPLICANT: Sareq, Hermona
APPLICANT: Shani, Mobile
TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTNACES
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: KOHN & ASSOCIATES
STREET: 30500 No. 6022183thwestern Highway, Suite 410
CITY: Farmington Hills
STATE: Michigan
COUTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: exon
LOCATION: 24090..25177
LIDENTIFICATION METHOD: experimental
OTHER INFORMATION: /function= "(translation start:
OTHER INFORMATION: /4110)"
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /gene= "ACHE"
OTHER INFORMATION: /gene= "ACHE"
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: promoter
LOCATION: 4089..22464
OTHER INFORMATION: /function= "ACHE Promotor"
OTHER INFORMATION: /standard_name= "ACHE Promotor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 48334

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/814,095
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Cosmid including ACHE
DESCRIPTION: promotor, ACHE gene and ARS gene"
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NAME/KEY: exon
LOCATION: 22465..2537
OTHER INFORMATION: /function="non-translated"
OTHER INFORMATION: /gene="AchtE"
OTHER INFORMATION: /number=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Wontgomery, ilene N.
REGISTRATION NUMBER: 38,972
REFERENCE/DOCKET NUMBER: 3391.00066
TELECOMMUNICATION INFORMATION:
TELEPHONE: (248) 539-5050
TELEFAX: (248) 539-5055
INFORMATION FOR SED ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 35060 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
  7351 TGAGCCAACGCGCCCAGAC 7369
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ORIGINAL SOURCE:
ORGANISM: Homo sapiens
POSITION IN GENÖME:
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Sequence 81, Application PC/TUS9306251

GENERAL INFORMATION:

TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing

TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:
                                                                                                                         1899 tttattatttatttatttattttactttttgagatagagtctcactcccttgctaaggc 1958
                                                           tttttttgagacaaagtctggctc-tgtcacccaggctggagtgcagtaatgcaatctca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 9.8%; Score 329.6; DB 5; Best Local Similarity 72.3%; Pred. No. 8.7e-70; Matches 518; Conservative 0; Mismatches 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: SCULLY, SCOTT, MURPHY & PRESSER 400 Garden City Plaza
2238 tgatttcacccttttatgtggatttacag-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Diddillo, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8586
TELECOMMUNICATION INFORMATION:
TELEFAN: 516-742-4343
TELEFAX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 81:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 841 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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COMPUTER READABLE FORM:
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; MOLECULE TYPE:
PCT-US93-06251-81
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 13
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OTHER INFORMATION: /gene= "AR"
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                                                                                                                                            LOCATION: complement (31363..31534)
OTHER INFORMATION: /gene= "AR"
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MATION: /number= 11
                                                             complement (31894..32080)
RMATION: /gene= "AR"
/gene= "AR"
/number= 8
                                                                                                 /number= 9
                                                      LOCATION: complemen OTHER INFORMATION: OTHER INFORMATION: FEATURE:
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OTHER INFORMATION:
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LOCATION: comp.
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LOCATION: comp.
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LOCATION:
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LOCATION:
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TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing
TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates
CORRESPONDENCES: 93
                                                                                                                                                                                                                                                              2295
                                                                                                                                                                                                                                                                                                             2336
                                                                   2019 ctccagcctcagcctccccaggtagctgggattacaagcatgcaccaccatgcctggata 2078
                                                                                                                                                                  ctgacctcaggtgatctgcctgcctcggcctccaaagtgctggaattacagatgtgagc 2198
                                                                                                                                                                                                                cactgtccctggcctggttacccacattttaaaatggagtgatttcacccttttatgtgg 2258
                                                                                  467
                                                                                                                                                                                                                                                                                                                                                                                                                   2517 cgccttggcctcccaaagtgctaggattacaggtgggaaccaccttgcccagcctg 2572
                                   2079 atttttgtatttttagttgagacggggtttcaccaggttggccagactggtctcgaactt
                                                                                                                               cagctcactgcaaccttagcctcctgggttcaagcaattctcctgcctcagccacctgag
                                                                                                                                                                                                                                                                                   409 GGTTAGTGCTTTTCACCCCTCGGGGGGGGGAGCTGCCAGACTTGGAATCTGACTC
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                                                                                                                                                                                                                                                                                                                                                                                289 CGGCTCACTGCAACCTCCCTCTCTCCCAAGTTCAAGTGATTCTCCTGCCTCAGCCTCCGAG
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tggagtgcggtggtgctatctcagctcactgcaacctctgcctcccaggatcaagtgatt
                                                                                                                                                                               57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER STREET: 400 Garden City Plaza CITY: Garden City
                                                                                                                                                                              atttacagcttgtttttttttttttgagacaaag.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: DiGiglio, Frank S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 19930630 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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PCT-US93-06251-80/c
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                                                                                                                                                                2139
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                       1959
                                             705
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1899 tttattatttatttatttattttacttttttgagatagagtctcactcccttgctaaggc 1958
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    526 CTGACCTCAGGTGATCCATCTGCCTCGGCCTCCCAAAGTGCTGGGATTACATGTGTAGGC
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Pred. No. 2.1e-69;
O; Mismatches 150;
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31,346
sR: 8586
                REFERENCE/DOCKET NUMBER: 856
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
TELEFAX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 80:
                                                                                                                                                                                                                                             ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US93-06251-80
                                                                                                                                                                                                                                                                                                                                                         9.8%;
                                                                                                                                                                        LENGTH: 841 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                Similarity
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Best Local Simi
Matches 517;
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JMBER: PCT/US95/07201
06-JUN-1995
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SYSTEM: PC-DOS/MS-DOS
WORDPERFECT 5.1
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FILING DATE: 30-DEC-1994
PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/257,963
FILING DATE: 07-JUN-1994
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ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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New York
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            APPLICANT: Chader, Gerald J.; Becerra, S.
APLICANT: Patricia; Schwartz, Joan P.;
APPLICANT: Patricia; Schwartz, Joan P.;
APPLICANT: Taniwaki, Takayuki
T.TLE OF INVENTION: DERIVED FOUTHELIUM
T.TLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION OF ITS NOVEL
TITLE OF INVENTION: BIOLOGICAL ACTIVITY AND SEQUENCES ENCODING
TITLE OF INVENTION: AND EXPRESSING THE PROTEIN
NIMBER OF SEQUENCES: 42
O'NRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64;
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fragment Derived from human placental
genomic DNA
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Pred. No. 8.9e-69;
0; Mismatches 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36434
REFERENCE/DOCKET NUMBER: 20264126US1
                                                                                                                                                                                                                                                                                                                                             SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/257,963B
                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
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                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 514
P\IOR APPLICATION DATA:
APPLICATION NUMBER: 07/952,7
FILING DATE: 24-SEPT-1992
AVTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 THECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 9:
SHOUENCE CHARACTERISTICS:
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Best Local Similarity 75.4%;
Matches 500; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1: 4421 Base Pairs
Nucleic Acid
DEDNESS: Double
                                                                                                                                                                                      345 Park Avenue
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unknown
                                                                                                                                                                                                       CITY: New York STATE: New York
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GENERAL INFORMATION:
                                                                                                                                                                                                                                         USA
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                                                                                                                                                                                                                                       COUNTRY: US
ZIP: 10154
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tgatctgcctgcctcggcctcccaaagtgctggaattacagatgtgagccactgtccctg 2209
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Sequence 9, Application PC/TUS9507201
GENERAL INFORMATION:
APPLICANT: Chader, Gerald J.; Becerra, Sofia
APPLICANT: Patricia; Schwartz, Joan P.;
APPLICANT: Taniwaki, Takayuki
TITLE OF INVENTION: PIGMENT EPITHELIUM
TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION GENOMIC
TITLE OF INVENTION: ORGANIZATION AND SEQUENCE OF THE PEDF GENE
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.

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4089 CAG 4091
                                             RESULT 11
US-09-009-913-1
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                                                                                                                                                                                                                                                                                                                                            DB 5; Length 4421;
                                                                                                                                                                                                                                                    7.1 kb Bam HI
fragment Derived from human placental
genomic DNA; Also referred to as JT101
                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                         cch 9.7%; Score 326.6; DB 5; al Similarity 75.4%; Pred. No. 8.9e-69; 500; Conservative 0; Mismatches 99;
         TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEPHONE: (212) 751-6849
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 4421 Base Pairs
TYPE: Nucleic Acid
STRANDEDNESS: Double
TOPOLOGY: UNKNOWN
                                                                                                                                               MOLECULE TYPE: Genomic DNA ORIGINAL SOURCE:
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                    LOCATION:
DENTIFICATION METHOD:
OTHER INFORMATION: frac
OTHER INFORMATION: gen
                                                                                                                                                                              ORGANISM: Human
                                                                                                                                                                                                           NAME/KEY: JT1
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Best Local Si
Matches 500;
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Db 47733 TITCATGAGACAAGGTCTTGCTCTGTTGCCCAGGCTGGAGTGCAGTGGCGTGATCTCTGC 47792
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGGGACTACAGGTGCGTGCCACCACAACCTGGCTAATTTTTGTATTTTTGGTAGAGATGG 47911
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Pred. No. 3.9e-67;
0; Mismatches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/^^C
CLASSIFITY
                                                                                                                                     APPLICANT: AxyS Pharmaceuticals, Inc. TTLE OF INVENTON: Asthma Related Genes NUMBER OF SEQUENCES: 339 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Bozicevic & Reed, LLP
STREET: 285 Hamilton Ave, Suite 200
; Sequence 1, Application US/09009913; Patent No. 6087485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Sherwood, Pamela J
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: SEQ-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-327-3231
TELEPAX: 650-327-3231
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Best Local Similarity 73.9%;
Matches 500; Conservative 0
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SEQUENCE CHARACTERISTICS:
LENGTH: 77228 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94301
COMPUTER READABLE FORM
MEDIUM TYPE: Disket
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: CA
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FEATURE:
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                                                                                                                                   48102 ACTGCAACCTCCGGCCTCCCAGGTTCAAGGGATTCTCCTGCCTCAGCCTTCCAAGTAG-CT 48160
                                                                                                                                                                                                                                                                                                                                         --GGTTTTTTTTTTT 48041
                                                                  Sequence 43, Application PC/TUS9507201

GENERAL INFORMATION:
APPLICANT: Chader, Gerald J.; Becerra, Sofia
APPLICANT: Tankaki, Taskyuki
TITLE OF INVENTION: DIGMENT EPTTHELLIUM
TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION GENOMIC
TITLE OF INVENTION: ORGANIZATION AND SEQUENCE OF THE PEDF GENE
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
CITY: New York
CITY: New York
                                                                                                                                                                                                                                                                          48219 GTTTCTTCATGTTGGTTAGGCTGGTCTCGAACTCCCAACCTCAGGTGATCTGCCCGCCTT
                                                                                                                 2343 actgcaaccttagcctcctgggttcaagcaattctcctgcctcagccacctgagtagcct
                                                                                                                                                                                                                                                     2523 ggcctcccaaagtgctaggattacaggtgggaaccaccttgcccagcctgtggctatcgt
tttgagacaaagtctggctc-tgtcacccaggctggagtgcagtaatgcaatctcagctc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07201
FILING DATE: 06-JUN-1995
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APPLICATION NUMBER: 08/367,841
FILING DATE: 30-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,963
FILING DATE: 07-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 07/952,796
FILING DATE: 24-SEP-1992
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: DOROTHY R. AUTH REGISTRATION NUMBER: 36434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                       48339 TTAAAACCATGAAACGC 48355
                                                                                                                                                                                                                                                                                                                                                                                        2583 ttaaacactgggaaggc 2599
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: New lot.
STATE: New York
COUNTRY: USA
ZIP: 10154
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13398 TCCTCGGCCTGCCAAAGTGCTGGGATTATAGGCCATAAGCCACTGCACCTAGCTCCCAATT 13457
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                                                                                                                                                                                                                                                                                                                    32;
                                                                                                                                                                                                                                                                           Score 321; DB 5; Length 22481;
Pred. No. 3.8e-67;
0; Mismatches 175; Indels 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IDENTIFICATION METHOD:
; OTHER INFORMATION: full length genomic
OTHER INFORMATION: sequence for PEDF plus flanking
PCT-US95-07201-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13458 ТТТАТАТТТАТАТТТТАТТТТТТТТАС----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-480-449-1; Sequence I, Application US/08480449; Patent No. 568897; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                           9.6%;
LENGTH: 22481 Base Pairs
TYPE: Nucleic Acid
STRANDEDNESS: Double
                                                                             MOLECULE TYPE: Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Godiska, Ronald
                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 70.6
Matches 498; Conservative
                                                             Unknown
                                                                                                                    NAME/KEY: Pl-147
LOCATION:
                                                             TOPOLOGY:
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REFERENCE/DOCKET NUMBER: 27866/33318
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STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/558,658
FILING DATE: 16-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/479,620
                                                                                                                                                                                                                                                                                                                                                           2561 ttgcccagcctgtggctatcgtt 2583
                                                                                                                                                                                                                                                                                                                                                                                              1810 ACACCCAGCCTCCCCTTTTTT 1832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 1, Application US/08660542; Patent No. 5932703; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A:
REGISTRATION NUMBER: 38,153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 2923 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
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                                                                       E: Marshall, O'Toole, Gerstein, Murray & Borun 6300 Sears Tower, 233 South Wacker Drive
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                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.5%; Score 318.6; DB 1; 70.5%; Pred. No. 6.2e-67; Live 0; Mismatches 184;
APPLICANT: Gray, Patrick W.
TITLE OF INVENTION: MACROPHAGE DERIVED CHEMOKINE
NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                 27866/32779
                                                                                                                                               COUNTRY: United States of America ZIP: 60606-6402
                                                                                                                                                                 ZIP: 60606-6402
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: GASS, DAVIG A:
REGISTRATION NUMBER: 38,153
REFRENCE/COCKET NUMBER: 2786/
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-6448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 2923 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Matches 524; Conservative
                                                      CORRESPONDENCE ADDRESS: ADDRESSEE: Marshall,
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                                                                                         STREET: 6300 Sec
CITY: Chicago
STATE: Illinois
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STRANDEDNESS:
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US-08-480-449-1
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                                                                           tgcagtaatgcaatctcagctcactgcaaccttagcctcctgggttcaagcaattctcct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
TITLE OF INVENTION: MACROPHAGE DERIVED CHEMOKINE AND CHEMOKINE
TITLE OF INVENTION: ANALOGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,542
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Memory T cell Trafficking

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Modulation of Systemic
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Best Local Similarity 70.55
Matches 524; Conservative
                                                                                ORGANISM: H. sapiens
                                                                                                  NAME/KEY: CDS
LOCATION: (20)
                                                                                                                            US-09-232-878-5
                                                                         TYPE: DNA
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                                                              Score 318.6; DB
Pred. No. 6.2e-67
0; Mismatches 18
                                                                                                                                                                                                                                                                                                                                 CAGTGCCTGGCC-------
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US-09-232-878-5
Sequence 5, Application US/09232878
Fatent No. 6245332
GENERAL INFORMATION:
APPLICANT: Butcher, Eugene
APPLICANT: Rutcher, James
APPLICANT: Rottman, James
APPLICANT: Wu, Lijan
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                                                             Ouery Match 9.5%;
Best Local Similarity 70.5%;
Matches 524; Conservative
                   mat_peptide
92..298
                ), NAME/KEY:
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US-08-660-542-1
LOCATION:
FEATURE:
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                                                                                                                                                                                                                                                     Length 2927;
                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                          LOCATION: (20)...(301)
OTHER INFORMATION: Coding sequence for MDC chemokine
                                                                                                                                                                                                                                                  Score 318.6; DB 4;
Pred. No. 6.2e-67;
0; Mismatches 184;
                                                                           3.0
                               US/09/232,878
; TITLE OF INVENTION: Modulation of System
; FILE REFERENCE: SUN-110PRY
; CURRENT PAPLICATION NUMBER: US/09/232,871;
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 6
; SSCHWARE: FEASLSEQ for Windows Version 3.
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70.58;
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Search completed: January 11, 2002, 12:08:49 Job time: 10881 sec

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January 11, 2002, 09:07:38 ; Search time 25.69 Seconds (without alignments) 2197.786 Million cell updates/sec
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2035
1 MGDTFIRHIALLGFEKRFVP......ADLILNRCSESTKRKLASAV 386
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Perfect score:
Sequence:
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473505 Total number of hits satisfying chosen parameters:

473505 seqs, 146272329 residues

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

SPTREMBL_17:* Database :

1: sp_archea:*
2: sp_barchea:*
3: sp_barchea:*
4: sp_buman:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
9: sp_organelle:*
9: sp_organelle:*
10: sp_organelle:*
11: sp_rodent:*
11: sp_rodent:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

CITMMAPTEC

					SUMMARIES	
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Result	Č	Query			;	
. So	Score	Match	Match Length DB	8 : BB	ID	Description
1	2023	99.4	390	4	Q9BU90	Q9bu90 homo sapien
7	2015	0.66	390	4	043842	043842 homo sapien
m	2005.5	98.6	389	4	6AGN6Ö	Q9udv9 homo sapien
4	1717.5	84.4	391	9	Q9N0E8	09n0e8 tursiops tr
S	1697	83.4	390	11	Q9J134	09ji34 mus musculu
9	1689.5	83.0	389	11	Ф39М65	099m65 rattus norv
7	1689	83.0	390	11	070144	O70144 mus musculu
8	1411	69.3		4	Q9BXI8	Q9bxi8 homo sapien
6	1346.5	66.2		11	Q9JK56	Q9jk56 rattus norv
10	1290	63.4		4	Q9BXI7	Q9bxi7 homo sapien
11	504.5	24.8	1124	11	089032	089032 mus musculu
12	334.5	16.4		4	Q9H462	Q9h462 homo sapien
13	275	13.5		4	043302	043302 homo sapien
14	197	7.6		9	Q9GMZ5	Q9gmz5 tursiops tr
15	188	9.5		4	Q9NZM2	_
16	188	9.5		4	Q9ULG4	homod
17	188	9.5		4	O9NYG0	O9nyg0 homo sapien
18	188	9.5	1696	4	O9NZM3	
19	185.5	9.1	550	4	Q9P2Q1	Q9p2q1 homo sapien

095062 homo sapien	O42287 xenopus lae	Q9bu98 homo sapien	Q9z0r5 mus musculu		Q15812 homo sapien	Q9z0r4 mus musculu	. Q9ntme homo sapien	Q9r143 mus musculu	Q9jlq0 mus musculu	Q9wve9 rattus norv	Q9unk1 homo sapien	Q9uet5 homo sapien	095216 homo sapien	Q9unk2 homo sapien	Q9y5k6 homo sapien	Q9d747 mus musculu	O61639 drosophila	O88903 mus musculu	O61618 drosophila	Q9wvel rattus norv	Q9vif7 drosophila	Q9uk60 homo sapien	Q9nyr0 homo sapien	091kgl rattus norv	P78815 schizosacch
095062	.3 042287	Q9BU98	1 0920R5	.1 Q9Z0R6	015812	.1 Q9Z0R4	9MTM60	.1 Q9R143	.1 09JLQ0	.1 Q9WVE9	Q9UNK1	Q9UETS	095216	Q9UNK2	Q9Y5K6	1 090747	061639	.1 088903	061618	1 09WVE1	09VIF7	Q9UK60	Q9NYR0	.1 09JKQ1	p78815
464 4	1270 1	348 4	1197 1	1658 1	248 4	1714 1	102 4	248 1	637 1	1217 1	1220 4	1220 4	1721 4	1721 4	639 4	239 1	1011 5	641 1	1094 5	1146 1	1097 5	187 4	665 4	585 1	290 3
9.0	8.8	8.7	8.7	8.7	8.7	8.5	8.3	8.3	8.3	8.2	8.2	8.2	8.2	8.2	8.1	8.1	8.1	7.9	7.9	7.9	7.8	7.4	7.4	7.4	7.2
183	179.5	178	177.5	177.5	176.5	172	169.5	168.5	168	166.5	166	166	166	166	164.5	164	164	161	161.	160.5	159.5	151	150.5	150	147.5
20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	. 45

ALIGNMENTS

RESULT 1	ID 098090 PRELIMINARY; PRT; 390 AA	NT 01-JUN-2001 (TrEMBLrel. 17, Created) NT 01-JUN-2001 (TrEMBLrel. 17, Last sequence undate)	01-JUN-2001 (TrEMBLrel. 17, Last annotation update)	DE NEUTROPHIL CYTOSOLIC FACTOR 1 (47KD, CHRONIC GRANULOMATOUS DISEASE,		Eukaryota; Metazoa; Chordata;	. Mammalia; Eutheria; Primates;	OX NCBI_TaxID=9606; RN [1] .	SEQUENCE FROM N.A.		Strausberg R.;	IL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. RMBL: BC002816: AAH02816 1: -		99.48;	<pre>Best Local Similarity 99.0%; Pred. No. 4.2e-153; Matches 386; Conservative 0; Mismatches 0; Indels 4; Gaps</pre>	н	Db 1 MGDTFIRHIALLGFEKRFVPSQHYVYMFLVKWQDLSEKVYRRFTEIYEFHKTLKEMFPI 60	61	Db 61 EAGAINPENRIIPHLPAPKWFDGQRAAENRQGTLTEYCSTLMSLPTKISRCPHLLDFFKV 120	Oy 121 RPDDLKLPTDNQTKKPETYLMPKDGKSTATDITGPIILQTYRAIANYEKTSGSEMALSTG 180	Db 121 RPDDLKLPTDNQTKKPETYLMPKDGKSTATDITGPILLQTYRAIANYEKTSGSEMALSTG 180	QY 181 DVVEVVEKSESGWWFCQMKAKRGWIPASFLEPLDSPDETEDPEPNYAGEPYVAIKAYTAV 240	AC TEMPORAL MANAGED AND AND AND AND AND AND AND AND AND AN	NATIVE AND TO A CONTRACT OF THE PROPERTY OF TH
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        RRSSIRNAHSIHQRSRKRLSQDAYRRNSVRFLQQRRRQARPGPQSPGSPLEEERQTQRSK 356
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EGDEVSLLEGEAVEVIHKLLDGW----KDDVTGYFPSMYLQKSGQDVSQAQRQIKRGAPP 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                        Craniata, Vertebrata, Euteleostomi;
Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-97474788; PubMed-9329953;
MEDLINE-97474788; PubMed-9329953;
Gorlach A. Lee P.L., Roesler J., Hopkins P.J., Christensen B.,
Green E.D., Chanock S.J., Curnutte J.T.;
"A p47-phox pseudogene carries the most common mutation causing
phox-deficient chronic granulomatous disease.";
J. Clin. Invest. 100:1907-1918(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                       Length 390;
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Last sequence update)
Last annotation update)
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98.5%; Pred. No. 1.8e-152;
ive 1; Mismatches 1;
                                                                                                              390 AA
                                                          357 PQPAVPPRPSADLILNRCSESTKRKLASAV 386
                                                                   361 PQPAVPPRPSADLILNRCSESTKRKLASAV 390
                                                                                                              PRT;
                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                           (TrEMBLrel. 06, TrEMBLrel. 06, (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                 44695
                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00312; PX; 1.
SMART; SM00326; SH3; 2
                                                                                                                                                                                                                                                                                                                                                                                          SH3;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                          PS50002;
                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                           01-JUN-1998 (
01-JUN-1998 (
01-JUN-2001 (
P47-PHOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 384;
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Gaps
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                                                                                                                                                            RRSSIRNAHSIHQRSRKRLSQDAYRRNSVRFLQQRRRQARPGPQSPGSPLEEERQTQRSK
                                                                   EGDEVSLLEGEAVEVIHKLLDGW----KDDVTGYFPSMYLQKSGQDVSQAQRQIKRGAPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 1e-151;
); Mismatches 0; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AC004883; AAD15422.1; -.
InterPro; IPR001452; SH3.
InterPro; IPR001655; P47PHOX.
InterPro; IPR001683; PX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The sequence of Homo sapiens PAC clone RP4-771P4.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Waterston R.H.;
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
WUGSC:H_DJ0771P04.4 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                          389 AA.
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Sulston J.E., Waterston R.;
"Town a complete human genome sequence.";
Genome Res. 8:1097-1108(1998).
                                                                                                                                                                                                                                                  PQPAVPPRPSADLILNRCSESTKRKLASAV 386
                                                                                                                                                                                                                                                                       PRT;
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Pfam; PF00018; S43; Z.
Pfam; PF00787; PX; 1.
PRINTS; PR004048; P47PHOX.
PRINTS; PR004048; P43DOMAIN.
PROSITE; PS50002; S43DOMAIN.
SWART; SW00312; PX; 1.
SWART; SW00326; S43; Z.
SEQUENCE 389 AA; 44584 MW;
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98.7%;
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Best Local Similarity 98.7
Matches 385; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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390 AA;
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01-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tursiops truncatus (Atlantic bottle-nosed dolphin).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
                                                                                                   DVVEVVEKSESGWWFCQMKAKRGWIPASFLEPLDSPDETEDPEPNYAGEPYVAIKAYTAV 240
RPDDLKLPTDNQTKKPETYLMPKDGKSTATDITGPIILQTYRAIANYEKTSGSEMALSTG 180
                       DVVEVVEKSESGWWFCQMKAKRGWIPASFLEPLDSPDETEDPEPNYAGEPYVAIKAYTAV 240
                                                                                                                                                                                 EAGAINPENRIIPHLPAPKWFDGQRAAENRQGTLTEYCSTLMSLPTKISRCPHLLDFFKV 120
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                                                                                                                                                              EGDEVSLLEGEAVEVIHKLLDGW----KDDVTGYFPSMYLQKSGQDVSQAQRQIKRGAPP 296
                                                                                                                                                                                                                                              RRSSIRNAHSIHORSRKRLSQDAYRRNSVRFLQQRRRQARPGPQSPGSPLEEERQTQRSK 356
                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Inoue Y., Itou T., Sakai T.;
"Molecular Cloning and Identification of Bottle-Nosed Dolphin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
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Pfam: PF00018; SH3; 2.
PRINTS: PR00459; PATPHOX.
SMART: SM00312; PX; 1.
SMART: SM00312; PX; 1.
SMART: SM00316; SH3; 2.
SPROSTIE: PS50002: SH3; 2.
SEQUENCE 391 AA; 44766 MW; F09E96D6B74B7C7C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          391 AA
                                                                                                                                                                                                                                                                                                                                               PQPAVPPRPSADLILNRCSESTKRKLASAV 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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InterPro; IPR001655; P47PHOX.
InterPro; IPR001683; PX.
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Interpro; IPR001452; SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 82.7
Matches 324; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9739;
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01-JUN-2001
P47-PHOX.
P47PHOX.
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181 DVVDVVEKSQSGWWFCQMKTKRGWVPASYLEPLDSPDEAEDPEPNYEGEPYITIEAYTAV 240
                                                                                                                                                           EAGAINPENRIIPHLPAPKWFDGQRAAENRQGTLTEYCSTLMSLPTKISRCPHLLDFFKV 120
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                                          1 MGDTFIRHIALLGFEKRFVPSQHYVYMFLVKWQDLSEKVVYRRFTEIYEFHKTLKEMFPI
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                                                                                                                                     RRSSIRNAHSIHORSRKRLSODAYRRNSVRFLOORRROARPGPOSPGSPLEEER--OTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Green E.D.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
R EMBL; AF26747; AF990134.1;
R MGD; MGI-97283; Ncfl.
R InterPro; IPR001655; P47PHOX.
R InterPro; IPR001655; P47PHOX.
R InterPro; IPR001683; PX.
R InterPro; IPR001455; SH3.
R Pfam; PF00787; PX; 1.
R Pfam; PF00787; PX; 1.
R PRINTS; PR00498; P47PHOX.
R PRINTS; PR00452; SH3DMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1697; DB 11; Length
Pred. No. 3.8e-127;
i; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MW; C8EFAB953839CE9A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                           390 AA
                                                                                                                                                                                                                           355 SKPQPAVPPRPSADLILNRCSESTKRKLASAV 386
                                                                                                                                                                                                                                                     34;
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81.18;
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Matches 317; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00312; PX; 1.
SMART; SM00326; SH3; 2.
PROSITE; PS50002; SH3; 3.
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RESULT Q99M65

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Mizuki K., Kadomatsu K., Hata K., Ito T., Fan Q.-W., Kage Y., Fukumaki Y., Sakaki Y., Takeshige K., Sumimoto H.; "Functional modules and expression of mouse p40(phox) and p67(phox), SH3-domain-containing proteins involved in the phagocyte NADPH oxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EAGAINPENRIIPHLPAPKWFDGQRAAENRQGTLTEYCSTLMSLPTKISRCPHLLDFFKV 120
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 Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 390;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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(TrEMBLrel. 17, Last annotation update)
EIN P47PHOX (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 1689; DB 11;
; Pred. No. 1.6e-126;
34; Mismatches 35;
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Eur. J. Biochem. 251:573:582(1998).
EMBL. AB002663; BAA25649.1; -.
MGD; MGI-97283; Ncf1.
InterPro; IPR001655; P47PHOX.
InterPro; IPR001653; PX.
InterPro; IPR001452; SH3.
Pfam; PF00787; PX; 1.
Pfam; PF00787; PX; 1.
Pfam; PF0018; SH3: 2.
PRINTS; PR00452; SH3: 2.
PRINTS; PR00452; SH3: 2.
PRINTS; SM00312; PX; 1.
SWART; SM00312; PX; 1.
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01-JUN-2001 (TrEMBLrel. 17, Last seq
01-JUN-2001 (TrEMBLrel. 17, Last ann
ADAPTOR PROTEIN P47PHOX (FRAGMENT).
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                                                                                 MEDLINE=98149672; PubMed=9490028;
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80.8%;
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Best Local Similarity 80.8%
Matches 316; Conservative
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                                                                                                                                                                                                                                                                                                                                                                           PS50002; SH3;
                                                                                                                                                                                                                                                                                                                                                                                           390 AA;
                NCBI_TaxID=10090;
                                                                TISSUE=LEUKEMIA;
                                                                                                                                                                                                                                                                                                                                                                            PROSITE;
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Q9BXI8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
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301 PRRSTIRNAQSIHQRSRKRLSQDTYRRNSVRFLQQRRRPGRPGPLSTDG-TKDNPSTPRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DVVEVVEKSESGWWFCQMKAKRGWIPASFLEPLDSPDETEDPEPNYAGEPYVAIKAYTAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EGDEVSLLEGEAVEVIHKLLDGW----KDDVTGYFPSMYLQKSGQDVSQAQRQIK-RGAP
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 11; Length 389;
                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=SPRAGUE-DAMLEY;
Tanabe M., Radmark O.P.;
"Full length sequence of rat p47 phox.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY029167; AAN13797.1;
EMBL; AY029167; AAN 44742 WW; BFC75842E53E68A4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33; Indels
                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
P47 PHOX.
Status norvegious (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83.0%; Score 1689.5; DB 11
81.1%; Pred. No. 1.5e-126;
Live 34; Mismatches 33;
                                                                                                                                               389 AA
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                                               360 KPQPAVPPRPSSDLILHRCTESTKRKLTSAV
                                356 KPQPAVPPRPSADLILNRCSESTKRKLASAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
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                                                                                                                                               PRT;
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07,
17,
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Best Local Similarity 81.14
Matches 317; Conservative
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                                                                                                                                                                                                                                                                                           NCBI_TaxID=10116;
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01-JUN-2001
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P47PHOX.

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241 241 296 301 356 359 us-09-820-005-2.rspt

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Matches 250;
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NON_TER
SEQUENCE
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Best Local 3
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                                                                                                                                                                                                                                                                                                           Ωy
                                                                                                                                                                                                                                                                                                                                                                                                    δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ΩŊ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 AIADYEKTSGSEMALSTGDVVEVVEKSESGWWFCQMKTKRGWIPASFLEPLDSPDETEDP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 EPNYAGEPYVAIKAYTAVEGDEVSLLEGEAVEVIHKLLDGWWVIRKDDVTGYFPSMYLQK 180
                                                                                                                                                                                                                                                                                                                                    103 SLPTKISRCPHLLDFFKVRPDDLKLPTDNQTKKPETYLMPKDGKSTATDITGPIILQTYR 162
                                                                                                                                                                                                                                                                                                                                                                                                                           AIANYEKTSGSEMALSTGDVVEVVEKSESGWWFCQMKAKRGWIPASFLEPLDSPDETEDP 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09JKS6;
01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-10T-2001 (TrEMBLrel. 17, Last annotation update):
P47PHOX (FRAGMENT).
Rattus norvegicus (Rat).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                           1 SLPTKISRCPHLLDFFKVRPDDLKLPTDNQTKRPETYLMPKDGKSTATDITGPIILQTYR 60
                                                                    oxidase.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ö.
                                                                                                                                                                                                                                             Length 276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schieffer B., Luchtefeld M., Hilfiker A., Hilfiker-Kleiner Drexler H.; "Role of NADPH oxidase in angiotensin II induced JAK/STAT activation.";
                               Gu Y., Xu Y., Souza R.F., Nwariaku F.E., Terada L.S.; "Activation of c-Jun amino terminal kinase by a signaling Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AR330225; AAK19516.1; -... 1

NON_TER 1

NON_TER 276 276

SEQUENCE 276 AA; 31332 MW; 7FAF4BF05C89E220 CRC64:
                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                           .;
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                                                                                                                                                                                                                                           Score 1411; DB 4;
Pred. No. 1.4e-104;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 PQSPGSPLEEERQTQRSKPQPAVPPRPSADLILINRC 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PQSPGSPLEEERQTQRSKPQPAVPPRPSADLILNRC 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        310 310
310 AA; 35798 MW;
                                                                                                                                                                                                                                           Query Match 69.3%;
Best Local Similarity 97.8%;
Matches 270; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66.2%;
80.6%;
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Pfam; PF00787; PX; 1.
Pfam; PF00018; SH3; 2.
PRINTS; PR00452; B47PHOX.
PRINTS; PR00452; SH3DOMAIN.
SMART; SM00312; PX; 1.
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Best Local Similarity
[1]
SEQUENCE FROM N.A.
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SEQUENCE
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TAKDGKNINVADIMGPIILQTYRAIADYEKGSKTEMTVATGDVVDVVEKSESGWWFCQMKP 180
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                                                                                                                                                                                                                                                   141 MPKDGKSTATDITGPIILQTYRAIANYEKTSGSEMALSTGDVVEVVEKSESGWWFCQMKA 200
                                                                                                                                                                                                                                                                                                                                                      201 KRGWIPASFLEPLDSPDETEDPEPNYAGEPYVAIKAYTAVEGDEVSLLEGEAVEVIHKLL 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         185 VVEKSESGWWFCQMKAKRGWIPASFLEPLDSPDETEDPEPNYAGEPYVAIKAYTAVEGDE 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 VVEKSESGWWFCQMKAKRGWIPASFLEPLDSPDETEDPEPNYAGEPYVAIKAYTAVEGDE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         245 VSLLEGEAVEVIHKLLDGW----KDDVTGYFPSMYLQKSGQDVSQAQRQIKRGAPPRRSS 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUE-UMPILICAL VEIN;
Gu Y., Xu Y., Souza R.F., Nwariaku F.E., Terada L.S.;
Activation of c-Jun amino terminal kinase by a signaling oxidase.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF330626; AAK19517.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 LKLPTDNQTKKPETYLMPKDGKSTATDITGPIILQTYRAIANYEKTSGSEMALSTGDVVE 184
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                        1 LKLPTDNQTKKPETYLMPKDGKSTATDITGPIILQTYRAIADYEKTSGSEMALSTGDVVE 60
                                                 SOHYVYMFLVKWODLSEKVVYRRFTEIYEFHKTLKEMFPIEAGAINPENRIIPHLPAPKW 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63.4%; Score 1290; DB 4; Length 254; 97.6%; Pred. No. 5.4e-95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
  28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134 134 E -> K.
254 254
254 AA; 28736 MW; FD7CC225ED7EDCF3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ADAPTOR PROTEIN P47PHOX (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 248; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 SODTYRRNSV 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SQDAYRRNSV 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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361 VPPRPSADLILNRC 374

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155 -PIILQTYRAIANYEKTSGSEMALSTGDVVEVVEKSESGWWFCQMKAKRGWIPASFLEPL 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             214 DSPDETEDPEPNYAG------EDYVAIKAYTAVEGD 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------RSSIRNAHSIHQRSRK 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             239 IGNIMEISNLLNKKASGDKETPPAEGEGHEAPIAKKEISLPILCNASNGSAVGVPDRTVS 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 LMSLPTKISRCPHLLDFFKVRPDDLKLP-TDNQTKKPETYLMPKDGKSTATDITG---- 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-001 (TrEMBLrel. 16, Last sequence update)
01-JUN-201 (TrEMBLrel. 17, Last annotation update)
BA416N2.2 (SIMILAR TO MRINE FISH (AN SH3 AND PX DOMAIN-CONTAINING PROTEIN, AND SRC SUBSTRATE)) (FRAGMENT).
                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EVSLLEGEAVEVIHKLLDGW-----KDDVTGYFPSMYLQKSGQDVSQAQRQI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ||:| : | : | : | | | RLAQGS--PAVARIAPQRAQISSPNLRTRPPP-RRESSLGFQLPKPPEPP 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 314 RLSQDAYRRNSVRFLQQRRRQARPGPQSPGSPLEEERQTQRSKPQPAVPP 363
                                                                                                                                                                                                                                                                                                                     Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL121929; CAC10184.1; -.
InterPror: IFRO1452; SH3.
Fram: PF000118; SH3; 5.
SMART: SM00326; SH3; 5.
PROSITE; PS50002; SH3; 5.
SMORTER: PS50002; SH3; 5.
SMORTER: SM00326; SH3; 5.
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16.4%; Score 334.5; DB 4; 25.4%; Pred. No. 4.2e-18; ive 58; Mismatches 110;
                                                      1031 AA
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06,
17,
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Chapman J.;
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SEQUENCE FROM N.A.
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ID 043302
                               Q9H462
ID Q9H462
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                  RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  246 AHLRRLDRRWTLGGMVNRQHSREEKYVTVQPYTSQSKDEIGFEKGVTVEVIRKNLEGWWY 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       363 AEGEGSEAPITKKEISLPILCNASNGSALAIPERTTSKLAQGS--PAVARIAPQRAQISS 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 DPKQRIIPFLPGKILFRRSHIRDVAVKRLKPIDEYCRALVRLPPHISQCDEVFRFFEARP 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 DDLKLP-TDNQTKKPETYLMPKDGKSTATDITG-----PIILQTYRAIANYEKTSGSEM 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---EPYVAIKAYTAVEGDEVSLLEGEAVEVIHKLLDGW-- 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            264 -----KDDVTGYFPSMYLQKSGQDVSQAQRQI---------KRGAP 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --RSSIRNAHSIHQRSRKRLSQDAYRRNSVRFLQQRRRQAR 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 NPENRIIPHLPAPKWFDGQR---AAENRQGTLTEYCSTLMSLPTKISRCPHLLDFFKVRP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 IRHIALLGFEKRFVPSQHYVYMFLVKWQDLSEKVVYRRFTEIYEFHKTLKEMFPIEAGAI 65
                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                176 ALSTGDVVEVVEXSESGWWFCQMKAKRGWIPASFLEPLDSPDETEDPEPNYAG-----
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                                                                                                                                                                                                                                                                                                                                        MEDLINE=98353460; PubMed=9687503;
Lock P., Abram C.L., Gibson T., Courtneidge S.A.;
"A new method for isolating tyrosine kinase substrates used
identify fish, an SH3 and PX domain-containing protein, and
substrate.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24.8%; Score 504.5; DB 11; Length 27.5%; Pred. No. 1.4e-31; ive 78; Mismatches 151; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13; 5.
124170 MW; 2A001B1D1CE98A67 CRC64;
                                                                                                                                                             Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                           EMBO J. 17.4346-4357(1998).
EMBL, AJ007012; CAA07416.1; -
MCD: MCI:129939; Fish.
InterPro; IPR001683; PX.
InterPro; IPR001452; SH3.
Pfam; PF00708; PX: 1.
Pfam; PF0018; SH3; 5.
SMART; SM00312; PX; 1.
PRONGTTE; PS50002; SH3; 5.
PROSTTE; PS50002; SH3; 5.
SEQUENCE F124 AA; 124170 MW;
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(TrEMBLrel. 08, 1
(TrEMBLrel. 17, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 27.5
Matches 123; Conservative
                                                                                                       PRELIMINARY;
241 VPPRPSADLILNRC 254
                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                 FISH PROTEIN.
                                                                                                                                           01-NOV-1998
01-NOV-1998
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                                                                                                       089032
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339 AA; 39363 MW; B6306ADD3D44E686 CRC64;

SEQUENCE

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                156 IILQTYRAIANYEKTSGSEMALSTGDVVEVVEKSESGWWFCQMKAKRGWIPASFLEPLDS 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        216 PDETEDPEPNYAG - - EPYVAIKAYTAVEGDEVSLLEGEAVEVIHKLLDGW - - - - - KDD 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -- GWAPASYLKKAKDDLPTRKKNLAGPVEIIGNIMEISNLLNKKASGDKETPPAEGEGHE 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----RSSIRNAHSIHQRSRKRLSQDAYRRNSVRFLQQRRRQARPGPQSPG 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ishikawa K., Nagase T., Nakajima D., Seki N., Ohira M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; ABO07878; BAA24481:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Inoue Y., Itou T., Sakai T.;
"Molecular Cloning and Identification of Bottle-Nosed Dolphin p40-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28;
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 13.5%; Score 275; DB 4; Length 940; Best Local Similarity 26.9%; Pred. No. 2e-13; Matches 70; Conservative 46; Mismatches 86; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases EMBL; AB038267; BAB11805.1; -..
InterPro; IPR00019; NCE_P40.
InterPro; IPR000108; Neu_cyt_fact_2.
InterPro; IPR000270; OPR.
InterPro; IPR000570; OPR.
                                                                                                                                                                                                                                                                                SMART; SM00326; SH3; 5.
SEQUENCE 940 AA; 102617 MW; 1CA24D7BC03BBAC3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUNY-2001 (TrEMBLrel. 17, Last annotation update)
p40-PHOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         339 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             344 SPLEEERQTQRSKPQPAVPP 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         236 PP-RRESSLGFQLPKPPEPP 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001452; SH3.
Pfam; PF00564; OPR: 1.
Pfam; PF00787; Px; 1.
Pfam; PF0018; SH3; 1.
PRINTS; PR00493; P67PHOX.
PRINTS; PR00499; P67PHOX.
PRINTS; PR00452; SH3DOMAIN.
SMART; SM00312; PX; 1.
SMART; SM00312; PX; 1.
PROSITE; PS50002; SH3; 1.
                                                                                                                                                  InterPro; IPR001452; SH3.
Pfam; PF00018; SH3; 5.
PRINTS; PR00452; SH3DOMAIN.
PROSITE; PS50002; SH3; 5.
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TISSUE=BRAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tursiops
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096M25
AC 096M25
AC 01-MAR
DT 01-MAR
DT 01-MAR
DT 01-JUN
DE P40-PBI
OC ENKATY
CO MAMMAN
OC ENKATY
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13;
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                                                                                                                                             117 ---FFKVRPDDLKLPTDNQTKKPETYLMPKDGKSTATDITGPIILQTYRAIANYEKTSGS 173
                                                                                                                                                                                                                                                     EMALS--TGDVVEVVEKSESGWWFCQMKAKRGWIPASFLEPLDSPDETEDP------ 222
                                                                                                                                                                                                                                                                                                                 Gaps
                                                             8 HIALLGFEKRFVPSQHYVYMFLVKWQDLSEKVVYRRFTEIYEFHKTLKEMFPIEAGAINP 67
                                                                                          25 NIADIEEKKGF--TSHFVFVIEVKTKGGSKYLIYRRYRQFYALQSKLEERF----GP 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

Pucharcos C., Estivill E., de la Luna S.;

"Cloning and characterization of human intersectin 2: a protein involved in endocytosis.";

Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.

-! - RIMILARITY: TO EF-HAND FAMILY.

EMBL; AF182199; AAF59904.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9.2%; Score 188; DB 4; Length 1248;
Length 339;
                              48; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Calcium-binding.
SEOUENCE 1248 AA; 141718 MW; A325BC186C76A97D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
9.7%; Score 197; DB 6; 25.7%; Pred. No. 8.4e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1248 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; TRE002048; EF-hand.
InterPro; IPR002048; EF-hand.
InterPro; IPR0010261; EPS15_repeat.
InterPro; IPR0010230; New_cyt_fact_2.
InterPro; IPR0010452; SH3.
IPRNTS; PR00409; P67PHOX.
INTER; PR000104; EFH; 2.
INMART; SM00027; EH; 2.
INMART; SM00027; EH; 2.
INMART; SM000264; EFH; 2.
INMART; SM00027; SH3. 5.
IPROSITE; PS000108; EF_HAND; UNKNOWN_I.
IPROSITE; PS00029; SH3; 5.
INTERPORTE; PS00029; SH3; 5.
INTERPORTE; PS00029; SH3; 5.
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                                                                                                                                                                                                                                                                                                                                                                             VIHKLLDG------WKDDVT 268
                                                                                                                                                                                                                                                                                                                                                                                                305 LMVKWTQGLPSQKHLFPWKLHIT 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2000 (TrEMBLrel, 15, 01-OCT-2000 (TrEMBLrel, 15, 01-JUN-2001 (TrEMBLrel, 17, INTERSECTIN 2 SHORT ISOFORM.
                              Conservative
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Query Match
Best Local Similarity
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                              83;
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Q9NZM2
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                                  Matches
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                                               228 -----GEPYVAIKAYTAVEGDEVSLLEGEAVEVIHKLLDGWK---DDVTGYFPSMYLQKS 279
Best Local Similarity 22.1%; Pred. No. 2.5e-06;
Matches 60; Conservative 58; Mismatches 102; Indels 52; Gaps
                                                                                                                                                                                                                             1037 DQESFGSAS--KSGASNKKPEIAQVTSAYVAS 1066
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Search completed: January 11, 2002, 09:11:05 Job time: 207 sec

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OM protein - protein search, using sw model

Run on:

January 11, 2002, 09:07:58 ; Search time 13.31 Seconds (without alignments) 1063.308 Million cell updates/sec

Title: Perfect score: Sequence:

US-09-820-005-2 2035 1 MGDTFIRHIALLGFEKRFVP......ADLILNRCSESTKRKLASAV 386

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

100059 seqs, 36664827 residues Searched:

100059 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P14598 homo sapien	bos t	Q09014 mus musculu	mus m	homo	homo	homo	mus m	000750 homo sapien	рошо	рошо	drosc				P42686 spongilla l	Q64096 mus musculu		Q04929 gallus gall		P33288 neurospora	. P40996 schizosacch		P34258 caenorhabdi	mus m		dicty		Spong	в ното за	3069 candi	7768 homo	P16333 homo sapien
SUMMARIES	QI	NCF1_HUMAN	NCF1_BOVIN	NCF1_MOUSE	NCF4_MOUSE	NCF4_HUMAN	ITSN_HUMAN	VINE_HUMAN	VINE_MOUSE	PK3B_HUMAN	SPCN_HUMAN	CRKL_HUMAN	SPCA_DROME	SPCN_CHICK	CRKL_MOUSE	FGR_MOUSE	SRK1_SPOLA	DBS_MOUSE	SLA1_YEAST	CRK_CHICK	MYSB_ACACA	UVS2_NEUCR	SCD2_SCHPO	YB65_SCHPO	YKA7_CAEEL	STAC_MOUSE	Y142_HUMAN	MYSD_DICDI	NCK2_HUMAN	SRK4_SPOLA	AMPH_HUMAN	CC25_CANAL	SNXG_HUMAN	NCK1_HUMAN
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	Score	2018	1754	1689	188.5	172.5	157	136.5	135.5	133.5	133.5	131.5	131.5	131.5	129.5	129.5	127.5	127.5	127	124	122	121.5	121	12	6	119.5		-	11	4	113.5	Э.		113
	Result No.		7	Э	4	2	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33

P00525 avian sarco P00523 gallus gall P14085 avian sarco P14084 avian sarco C64010 mus musculu C63768 rattus norv C93768 rattus norv C93778 xenopus lae P87378 xenopus lae P46108 homo sapien C09126 mus musculu
SRC_AVISR SRC_CHICK SRC_AVIST SRC_AVISS SRC_AVISS SRC_AVISS CRK_MOUSE CRK_RAT STRC_HUMAN YHR4_YEAST CRK_EULA CRK_EULAN SM4D_MOUSE
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525 5326 5532 5532 304 304 861
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113 113 113 113 111.5 111.5 110.9.5 109.5
44444 93 93 93 93 94 94 95 95 95 95 95 95 95 95 95 95 95 95 95

## ALIGNMENTS

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RSKPQPAVPPRPSADLILNRCSESTKRKLASAV 386
     Bovinae; Bos.
    Bovidae; Bovinae
NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                 SH3 domain
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RRSSIRNAHSIHQRSRKRLSQDAYRRNSVRFLQQRRRQARPGPQSPGSPLEEERQTQRSK 356
                                                                                                                                                                                                                                                                                                                                                        EAGAINPENRIIPHLPAPKWFDGQRAAENRQGTLTEYCSTLMSLPTKISRCPHLLDFFKV 120
                                                                                                                                                                                                                                                                                                                                                                                               121 RPDDLKLPTDNQTKKPETYLMPKDGKSTATDITGPIILQTYRAIANYEKTSGSEMALSTG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                      DVVEVVEKSESGWWFCQMKAKRGWIPASFLEPLDSPDETEDPEPNYAGEPYVAIKAYTAV 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EGDEVSLLEGEAVEVIHKLLDGW----KDDVTGYFPSMYLQKSGQDVSQAQRQIKRGAPP 296
                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                           30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
20-MOG-2001 (Rel. 40, Last annotation update)
NEUTROPHIL CYTOSOL FACTOR 1 (NCF-1) (NEUTROPHIL NADPH OXIDASE FACTOR 1) (47 KDA NEUTROPHIL OXIDASE FACTOR) (P47-PHOX) (NCF-47K).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                  1 MGDTFIRHIALLGFEKRFVPSQHYVYMFLVKWODLSEKVVYRRFTEIYEFHKTLKEMFPI
                                                                                                                                                                                                                                                                                                4;
                                                                                                                                                                                                                                                                           Length 390;
                                                                                                                                                                                                    ASP/GLU-RICH (HIGHLY ACIDIC).
ARG/LYS-RICH (HIGHLY BASIC).
                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                             B11B256516F3AA9B CRC64;
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                                                                                                                                                                                                                                                                          99.2%; Score 2018; DB 1; 98.7%; Pred. No. 1.4e-140; ive 1; Mismatches 0;
                                                                            InterPro; IPR001655; P47PHOX.
InterPro; IPR001653; PX.
InterPro; IPR00163; PX;
InterPro; IPR001645; SH3.
Pfam; PF00787; PX; 1.
Pfam; PF00018; SH3; 2.
PRINTS; PR00498; P47PHOX.
SMART; SM0312; PX; 1.
SMART; SM0312; PX; 1.
SMART; SM0312; PX; 1.
SMART; SM0312; SH3; 2.
SMART; SM0312; SH3; 2.
SMART; SM0312; SH3; 2.
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                                                                                                                                                                                                                         SH3
SH3
                                                                                                                                                                                                                                              WW.
                                       EMBL; M25665; AAA57209.1; -. EMBL; M55067; AAA59901.1; -. PIR; A39249; A39249. MIM; 233700; -.
                                                                                                                                                                                                                                             44682
                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 98.7
Matches 385; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                              390
215
285
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390 AA;
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077774:
                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 2
NCFL_BOVIN
ID AC 077774
DT 30-MAY
DT 20-AUG
DE NEUTRO
DE NEUTRO
DE NEUTRO
DE NEUTRO
GN NCFL'
GN MADMWAI
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 ;
Bunger P.L., Siemsen D., Quinn M.T.;
Bunger P.L., Siemsen D., Quinn M.T.;
"Cloning and expression of bovine NADPH oxidase proteins p47-phox and p67-phox.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: NCF2, NCF1, AND A MEMBRANE BOUND CYTOCHROME B558 ARE REQUIRED FOR ACTIVATION OF THE LATENT NADPH OXIDASE (NECESSARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 EAGAINPENRIIPHLPAPKWFDGQRAAENRQGTLTEYCSTLMSLPTKISRCPHLLDFFKV 120
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ASP/GLU-RICH (HIGHLX ACIDIC).
ARG/LYS-RICH (HIGHLY BASIC).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86.2%; Score 1754;
85.0%; Pred. No. 3e-
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InterPro; IPR001655; P47PHOX.
InterPro; IPR001683; PX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001452; SH3.
Pfam; PF00787; PX; 1.
Pfam; PF00018; SH3. 2.
PRINTS; PR00452; SH3DMAIN.
PRINTS; PR00498; P47PHOX.
SMART; SM00312; PX; 1.
SMART; SM00326; SH3; 2.
PROSITE; PS50002; SH3; 2.
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Matches 334; Conservative
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292
156
226
392 AA;
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Matches 316;
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P97369;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mizuki K., Kadomatsu K., Hata K., Ito T., Fan Q.-W., Kage Y.,
Fukumaki Y., Sakaki Y., Takeshige K., Sumimoto H.;
"Functional modules and expression of mouse p40(phox) and p57(phox),
SH3-domain-containing proteins involved in the phagocyte NADPH oxidase
                                                                                        NCFL MOUSE STANDARD; PRT; 390 AA.

009014; 070144; 09J134;
01-NOV-1995 [Rel. 32, Created)
20-AUG-2001 [Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
NEUTROPHIL CYTOSOL FACTOR 1 (NCF-1) (NEUTROPHIL NADPH OXIDASE FACTOR 1) (47 KDA NEUTROPHIL OXIDASE FACTOR)
NCF1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Green E.D.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: NCF2, NCF1, AND A MEMBRANE BOUND CYTOCHROME B558 ARE REQUIRED FOR ACTIVATION OF THE LATENT NADPH OXIDASE (NECESSARY FOR SUPEROXIDE PRODUCTION).
                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_raxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-94164697; Pubmed-8119734;
Jackson S.H., Malech H.L., Kozak C.A., Lomax K.J., Gallin J.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Holland S.M.; "Cloning and functional expression of the mouse homologue of p47phox.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PX.
ASP/GLU-RICH (HIGHLY ACIDIC).
ARG/LYS-RICH (HIGHLY BASIC).
360 RPKPQPAVPPRPSADLILHRCSESTKRKLASAV 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELULAR LOCATION: CYTOPLASMIC. SIMILARITY: CONTAINS 2 SH3 DOMAINS. SIMILARITY: CONTAINS 1 PX DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98149672; PubMed=9490028;
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EMBL; AF267747; AAF90134.1; -.
MGD; MGI: 97263; Ncf1.
InterPro; IPR001655; P47PHOX.
InterPro; IPR001653; PX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunogenetics 39:272-275(1994).
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Pfam: PF00787; PX: 1.
Pfam: PF00018: SH3; 2.
PRINTS; PR00498; P47PHOX.
PRINTS; PR00498; P47PHOX.
SMART; SM00312; PX: 1.
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SH3 domain.
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254
390
                                                                                                                                                                                                                                                                              musculus (Mouse)
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TISSUE=Macrophage;
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                                                           SULT 3
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Mizuki K., Kadomatsu K., Hata K., Ito T., Fan Q.-W., Kage Y., Fukumaki Y., Sakaki Y., Takeshige K., Sumimoto H.; "Functional modules and expression of mouse p40(phox) and p67(phox), SH3-domain-containing proteins involved in the phagocyte NADPH oxidase
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-!- FUNCTION: COMPONENT OF THE NADPH-OXIDASE, A MULTICOMPONENT ENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EAGAINPENRIIPHLPAPKWFDGQRAAENRQGTLTEYCSTLMSLPTKISRCPHLLDFFKV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
40 (Rel. 270:SOL FACTOR 4 (NCF-4) (NEUTROPHIL NADPH OXIDASE FACTOR 4) (P40:PHOX) (P40:PHOX)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                       Length 390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
SH3 1.
SH3 2.
Y -> H (IN REF. 1).
GQL -> RAA (IN REF. 1).
Q -> P (IN REF. 3).
W; A383DB953839CFCB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                             ; Score 1689; DB 1; ; 
; Pred. No. 1.7e-116; 
34; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           339 AA
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MEDLINE=98149672; PubMed=9490028;
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80.8%;
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285
161
345
344
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SEQUENCE FROM N.A.
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Q15080; O60808; Q9NP45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10;
                 TRANSPORTED FROM NADPH TO MOLECULAR OXYGEN, GENERATING REACTIVE OXIDANT INTERMEDIATES. IT MAY BE IMPORTANT FOR THE ASSEMBLY AND/OR ACTIVATION OF THE NADPH-OXYDASE COMPLEX.
SUBUNIT: P40-PHOX ASSOCIATES PRIMARILY WITH P67-PHOX TO FORM A COMPLEX WITH P47-PHOX.
SYSTEM RESPONSIBLE FOR THE OXYDATIVE BURST IN WHICH ELECTRONS ARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134 KKPETYLMPKDGKSTATDITGPII--LQTYRAIANYEKTSGSEMALS--TGDVVEVVEKS 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                190 ESGWWFCQMKAKRGWIPASFLEPLDSPDETEDP-------EPNYAG 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 204 NKDWLEGTSQGATGIFPGSFVKILKDFPEDEDTTNWLRCYFYEDTGKTIKDIAVEEDLSS 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          229 EPY-----VAIKAYTAVEGDEVSLLEGEAVEVIHKLLDG-----W 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EKRFVPSQHYVYMFLVKWQDLSEKVVYRRFTEIYEFHKTLKEMFPIEAGAINPENRIIPH 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62C4B3252D2C4B98 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.3%; Score 188.5; DB 1;
26.2%; Pred. No. 8.2e-07;
Live 40; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     339 AA.
                                                                                                                  SUBCELLULAR LOCATION: CYTOPLASMIC. SIMILARITY: CONTAINS 1 SH3 DOMAIN. SIMILARITY: CONTAINS 1 PX DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PX.
SH3
                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P29355; 2SEM.
MGD; MGI:109186; NcF4.
InterPro; IPR000919; NCF_P40.
InterPro; IPR000270; OPR.
InterPro; IPR001683; PX.
InterPro; IPR001452; SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           339 AA; 38734 MW;
                                                                                                                                                                                                                                                                                                                                                                       EMBL; U59488; AAC53122.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00452; SH3DOMAIN.
PRINTS; PR00497; P40PHOX.
SMART; SW00016; OPP; 1.
SMART; SW00312; PX; 1.
SMART; SW00326; SH3; 1.
PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 26.2°,
Local 80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                              AB002665; BAA25651.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00564; OPR; 1.
Pfam; PF00787; PX; 1.
Pfam; PF00018; SH3; 1.
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NCF4_HUMAN
•ID NCF4_HI
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RA MEDLINES_2009.105; FUDMEDE_1009.1208;
RA MEDLINES_2009.105; FUDMEDE_1009.1208;
RA Blagguley C., Bailey J., Bailogo A., Babage A.,
RA Bagguley C., Bailey J., Barlow K., Bates K.N., Beasley O., Bird C.P.,
Blagguley C., Bailey J., Barlow K., Bates K.N., Bearlil W.D.,
Blagguley C., Bailey J., Barlow K., Bates K.N., Bearlil W.D.,
RA Burton J., Carder C., Carter N.P., Chen Y., Clark G., Clegg S.M.,
Cobley V., Cole C.G., Collier R.E., Connor R.E., Conroy D., Corby N.,
Colley G.J., Cox A.V., Davis J., Dawson E., Dhami P.D., Dockree C.,
RA Graffbam D., Griffiths M., Ballington A., Evans K.L., Fey J.M.,
RA Graffbam D., Griffiths M.N., Hall C., Hall R., Hall-Tamlyn G.,
Heathcott R.W., Ho S., Holmes S., Hunt S.E., Jones M.C., Kershaw J.,
RA Kimberley A., King A., Lald G.K., Langford C.F., Leversha M.A.,
RA Milles S.A., Mortamo J.T., Mashreghi-Mohammadi M.,
Matthews L., Mocann O. J., Molaren S., Meunray A.A.,
Milles S.A., Mortimore B.J., Phillings S.H., Plumb R.W., Skuce C.D.,
Smalley C., Lloyd D.M., Marryn I.D., Mashreghi-Mohammadi M.,
RA Smalley S., Smith M.L., Soderlund C., Spragon L., Steward C.A.,
Sulston J.E., Swann R.M., Vaudin M., Wallis J.M.,
RA Smalley S., Smith M.L., Soderlund C., Spragon L., Steward C.A.,
Sulston J.E., Swann R.M., Vaudin M., Walliams S., Williams S., Williams S., Williams S., Williams S., Williams S., Rawasaki K., Sasaki T.,
Beck S., Rogers J., Shintani A., Shibuya K., Yoshizaki Y., Aoki N.,
Mitsuyama S., Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S.
Doan D., Song L., Wang P., Wall S., Lin S.P., Loh P., Bradshaw H.,
Minx P., Fulton R., Jang F., Williams S., White J., Waller S.,
RA, Bourne S., Cockes M., Johnson D., Benis G., Bentley D., Bradshaw H.,
RA, Bourne S., Cockes M., Johnson D., Benis G., Bentley D., Bradshaw H.,
RA, Budarf M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E.,
RA, Budarf M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wientjes F.B., Hsuan J.J., Totty N.F., Segal A.W.; "p40phox, a third cytosolic component of the activation complex of the NADPH oxidase to contain src homology 3 domains."; Biochem. J. 296:557-561(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
MEDLINE-99384495; DAMPEd-10437784;
HASSEDE T., Someya A., Nagaoka I.;
"Identification of a splice variant mRNA of p40phox, an NADPH oxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhan S., Vazquez N., Zhan S., Wientjes F.B., Budarf M.L., Schrock E., Ried T., Green E.D., Chanock S.J., "Genomic structure, chromosomal localization, start of transcription,
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MG-2001 (Rel. 40, Last annotation update)
NEUTROPHIL CYTOSOL FACTOR 4 (NCF-4) (NEUTROPHIL NADPH OXIDASE FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and tissue expression of the human p40-phox, a new component of the nicotinamide adenine dinucleotide phosphate-oxidase complex.";
                                                                                                                                                                                                                                                                                                                                   Euteleostomi;
                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-94107216; PubMed-8280052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=20057165; PubMed=10591208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=96437051; Pubmed~8839867;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             component of phagocytes."; FEBS Lett. 455:257-261(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Blood 88:2714-2721(1996).
                                                                                                                                                                                            (P40-PHOX) (P40PHOX)
                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
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RESULT
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                                                                                                                  TRANSPORTED FROM NADPH TO MOLECULAR OXYGEN, GENERATING REACTIVE OXIDANT INTERMEDIATES. IT MAY BE IMPORTANT FOR THE ASSEMBLY AND/OR ACTIVATION OF THE NADPH-OXYDASE COMPLEX.
SUBGUNIT: P40-PHOX ASSOCIATES PRIMARLLY WITH P67-PHOX TO FORM A SUBGULLULEX WITH P47-PHOX.
SUBGLELLULEX ELCALION: CYTOPLASMIC.
ALLERRATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APSGSQMSHNAVTSHQRPGWPGQPHSPFPHPTPHFQPDASL
LQPVTPLGTSRWRKISAALPY (IN ISOFORM 2).
9A099ACOE834F9OC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DIAVEEDLSSTPLLKDLLELTRREFQREDIALNYRDAEGDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -> SVAWEGGACPAFLPSLRPPPLTSPSHGSLSHSK
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                                                                                      FUNCTION: COMPONENT OF THE NADPH-OXIDASE, A MULTICOMPONENT ENZYME SYSTEM RESPONSIBLE FOR THE OXYDATIVE BURST IN WHICH ELECTRONS ARE
Edelmann L., Kim U.J., Shizuya H., Simon M.I., Dumanski J.P., Peyrand M., Kedra D., Seroussi E., Fransson I., Tapia I., Bruder C.E. O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X., Khan A.S., Lane L., Tilahun Y., Wright H.,
                                                                                                                                                                                                                                           TISSUE SPECIFICITY: EXPRESSION IS RESTRICTED TO HEMATOPOIETIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  I -> L.
/FTId=VAR_009314.
                                                          "The DNA sequence of human chromosome 22.";
                                                                                                                                                                                                                                                                        SIMILARITY: CONTAINS 1 SH3 DOMAIN. SIMILARITY: CONTAINS 1 PX DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      , U50720; AAB39970.1; JOINED.
1 U50721; AAB39970.1; JOINED.
1 U50723; AAB39970.1; JOINED.
1 U50723; AAB39970.1; JOINED.
1 U50724; AAB39970.1; JOINED.
1 U50725; AAB39970.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              U50726; AAB39970.1; JOINED.
U50727; AAB39970.1; JOINED.
U50728; AAB39970.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AB025220; BAA89792.1; -. AB025219; BAA89791.1; -. AL008637; CAA15486.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000919; NCF_P40.
InterPro; IPR000270; OPR.
InterPro; IPR001683; PX.
                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U50729; AAB39970.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAA54372.1;
                                                                        Nature 402:489-495(1999).
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Pfam; PF00018; SH3; 1.
PRINTS; PR00497; P40PHOX.
SMART; SM00116; OPR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00312; PX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001452;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00326; SH3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P29355; 3SEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        339 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  147
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EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP;
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12;

Gaps

71;

Indels

8.5%; Score 172.5; DB 1; Length 339; 24.4%; Pred. No. 1.2e-05;

48; Mismatches 116;

76; Conservative

Query Match Best Local Similarity Matches 76; Conserv

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                                                                                                                                                                                                                                                                                        KLPTDNQTKKPETYLMPKDGKSTATDITGPIILQTYRAIANYEKTSGSEMALS--TGDVV 183
                                                                                                                                                                                                                                                                                                                                     258 EEDLSSTPLLKDLLELTRREFQREDIALN-YRDAEGDLVRLLSDEDVALMVRQARGLPSQ 316
                                                                                                                                          --IIPHLPAPKWFDG--QRAAENRQGTLTEYCSTLMSLPTKISRCPHLLDFFKVRP-DDL 125
                                                                                                                                                                                       EKRFVPSQHYVYMFLVKWQDLSEKVVYRRFTEIYEFHKTLKEMFPIEAGAINPENR---- 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Bone marrow;
MEDLINE=98294438; PubMed=9630982;
Sparks A.B., Hoffman N.G., McConnell S.J., Fowlkes D.M., Kay B.K.;
"Cloning of ligand targets: systematic isolation of SH3 domain-
                                            ||| | |:|:: || : ::|||: :
EKRGFTS-HFVFVIEVKTKGGSKYLIYRRYRQFHALQSKLEERF-----GPDSKSSAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----VAIKAYTAVEGDEVSLLEGEAVEVI------H
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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"The SH3DIA gene maps to human chromosome 21q22.1-->q22.2.";
Cytogenet. Cell Genet. 78:213-215(1997).
-! SIMILARITY: CONTAINS 4 SH3 DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                  184 EVVEKSESGWWFCOMKAKRGWIPASFLEPLDSPDETEDP-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
INTERSECTIN (SH3 DOMAIN-CONTAINING PROTEIN SH3P17).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     520 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biotechnol. 14:741-744(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=98127038; PubMed=9465890;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last seq
15-JUL-1999 (Rel. 38, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U61166; AAC50592.1; -. HSSP; P29354; 1GFD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00452; SH3DOMAIN.
SMART; SM00326; SH3; 4.
PROSITE; PS50002; SH3; 4.
SH3 domain; Repeat.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001452; SH3.
Pfam; PF00018; SH3; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              317 KRLFPWKLHIT 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                containing proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EPNYAGEPY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ITSN OR SH3D1A.
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Q15811;
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15
                                                                                                                                                                                                                                                                                        126
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us-09-820-005-2.rsp

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CONFLICT
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Best Local 3
                                                                                                                                                                                                                                                                                                                                                                                                                   VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kioka N., Sakata S., Kawauchi T., Amachi T., Akiyama S.K., Okazaki K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Vinexin forms a signaling complex with Sos and modulates epidermal growth factor-induced c-Jun N-terminal kinase/stress-activated protein kinase activities.";
J. Biol. Chem. 274:35933-35937(1999).
-!- FUNCTION: VINEXIN ALPHA ISOFORM PROMOTES UPREGULATION OF ACTIN STRESS FIBER PORMATION. VINEXIN BETA ISOFORM PLAYS A ROLE IN CELL SPREADING AND ENHANCES THE ACTIVATION OF JNK/SAPK IN RESPONSE TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE EXCHANGE FACTOR OF RAS AND RAC), THROUGH ITS THIRD SH3
DOMAIN. THE FORMATION OF THIS COMPLEX IS DOWN-REGULATED BY
PHOSPHORYLATION OF SOS.

-1- SUBCELLULAR LOCATION: BOTH ISOFORMS WERE LOCALIZATED AT FOCAL
ADHESION AND CELL-CELL ADHESIONS SITES, VINEXIN BETA WAS ALSO
FOUND IN THE NUCLEUS.
-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA (SHOWN HERE) AND BETA; ARE
PRODUCED BY ALTERNATIVE SPLICING.
-1- TISSUE SPECIFICITY: BOTH ISOFORMS ARE EXPRESSED IN DIFFERENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EGF STIMULATION BY USING ITS THIRD SH3 DOMAIN.
SUBUNIT: INTERACTS WITH VINCULIN BY THE FIRST TWO SH3 DOMAINS AND
THE PROLINE RICH REGION OF VINCULIN. BINDS TO SOS (GUANINE
                                                                                                                                                    418 ARGKKRQIGWFPANYVKLL-SPGTSKITPTEPPKSTALAAVCQVIGMYDYTAQNDDELAF 476
                                                                                                                                   142 PKDGKSTATDITGPIIL--QTYRAIANYEKTSGSEMALSTGDVVEVVEKSESGWWFCQMK 199
                                                                                                                                                                                      A---KR--GWIPASFLEPLDSP-----DETEDPEPNYAGE--PYVAIKAYTAVEGDEVSL 247
                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yaen C., Yamada K.M., Aota S.-I.;
"Vinexin: a novel vinculin-binding protein with multiple SH3 domains enhances actin cytoskeletal organization.",
J. Cell Blol. 144:59-69(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-20054482; Pubmed-10585480;
Akamatsu M., Aota S.-I., Suwa A., Ueda K., Amachi T., Yamada K.M.,
Akiyama S.K., Kioka N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                          20;
                                                                              Length 520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND MUTAGENESIS
                                                                                                          61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [2]
SEQUENCE FROM N.A. (ISOFORM ALPHA).
Her J.-H., Gorman D., Miyajima A., Bolen J.B.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
SH3 2.
SH3 3.
SH3 4.
: 614043FlDB098C60 CRC64;
                                                                                                                                                                                                                                                                                                                                                              20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
VINEXIN (SH3-CONTAINING ADAPTOR MOLECULE-1) (SCAM-1).
                                                                                                                                                                                                                                                          :|::|::||||:||477 NKGQIINVLNKEDPDWWKGEVNGQVGLFPSNYVKLTTDMDPSQ 519
                                                                                                                                                                                                                                           248 LEGEAVEVIHKL-LDGWKDDV---TGYFPSMYLQ-KSGQDVSQ 285
                                                                             7.7%; Score 157; DB 1;
28.8%; Pred. No. 0.00029;
iive 35; Mismatches 61
                                                                                                                                                                                                                                                                                                                                      671 AA
                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Placenta;
MEDLINE=99102423; PubMed=9885244;
 342 SH
438 SH
514 SH
57976 MW;
                                                                      Query Match
Best Local Similarity 28.89
                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERACTION WITH SOS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                    O60504; Q9UQE4;
                                                                                                                                                                                                                                                                                                                                      VINE_HUMAN
                           DOMAIN
SEQUENCE
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the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19;
                                                                                                                                              EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cell adhesion; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EIYEFHKTL-KEMFPIEAGAINPENRIIPHLPAPKWFDGQRAAENR--QGTLTEYCSTLM 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SLP---TKISRCPHLL------DFFKVRPDDLKLPTDNQTKKPETYLMPKDGKST 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          328 HAPYLGSARSLSPHKMADGGSPFLGRRDF--VYPSSTRDPSASNGGGSPARREEKKRKAA 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 149 ATDITGPIILQTYRAIANYEKTSGSEMALSTGDVVEVVEKSESGWWFCQMKAKRGWIPAS 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 209 FLEPLDSPDETEDP--EPNYAGEPYVAIKAYTAVEGD---EVSLLEGEAVEVIHKLLDGW 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                264 KDD-VT----GYFPSMYLQKSGQDVSQAQRQIKRGAPPRRSSIRNAHSIHQRSRKRLSQ 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DAYRRNSVRFLQQRRRQARPGPQSPGS----------PLEEER-QTQ 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----VSREPRLRLCD 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | : ; | | | | | | | | | DEPQLPTSPRETGESFPTGEPRPQED 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 111; Gaps
TISSUES LIKE HEART, PLACENTA, BRAIN, SKELETAL MUSCLE AND PRANCREAS. VINEXIN BETA ISOFORM IS ESPECIALLY FOUND IN LIVER. SIMILARITY: CONTAINS 3 SH3 DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MISSING (IN ISOFORM BETA).
W->F: LOSS OF SOS-BINDING ABILITY.
Y->V: LOSS OF SOS-BINDING ABILITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                           the Swiss Institute of Bioinformatics and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L -> F (IN REF. 1).
7D978711726BCD32 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 136.5; DB 1;
Pred. No. 0.013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Repeat; Cell adhesion; SORB.
SNB 1.
SNB 2.
SNB 3.
SNB 3.
BINDS TO VINCULIN.
BINDS TO SOS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R-SKPQPAVPPR--PSADLILNRCSESTKR 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          582 NLGTPGPALSHSRGPSHPLDLGTSSPNTSQ 611
                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P07751; 1BK2.
InterPro; IPR00108; Neu_cyt_fact_2.
InterPro; IPR001452; SH3.
InterPro; IPR003157; Sorb.
Pfam; PF00108; SH3; 3.
Pfam; PF02208; Sorb; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51;
                                                                                                                                                                                                                                                                                                                                        EMBL; AF04807; AAD32304.1; -. EMBL; AF037261; AAC09244.1; -.
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M
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22.6%;
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SMART; SM00326; SH3; 3.
SMART; SM00459; Sorb; 1.
PROSITE; PS50002; SH3; 3.
Cytoskeleton; SH3 domain; Rep
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             671 AA;
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322
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                                                                                                                                                                                                                                                      Kioka N., Sakata S., Kawauchi T., Amachi T., Akiyama S.K., Okazaki K., Yaen C., Yamada K.M., Aota S.-I.;
"Vinexin: a novel vinculin-binding protein with multiple SH3 domains enhances actin cytoskeletal organization.";
J. Cell Biol. 144:59-69(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                      containing proteins.":

Nat. Blotechnol. 14:741-744(1996).

Nat. Blotechnol. 14:741-744(1996).

-!- FUNCTION: PROMOTES UPREGULATION OF ACTIN STRESS FIBER FORMATION.

-!- SUBUNIT: INTERACTS WITH VINCULIN BY THE FIRST TWO SH3 DOMAINS AND THE PROLITE RICH REGION OF VINCULIN. BINDS TO SOS (GUANINE NUCLEOTIDE EXCHANGE FACTOR), THROUGH ITS THIRD SH3 DOMAIN. THE FORMATION OF THIS COMPLEX IS DOWN-REGULATED BY PHOSPHORYLATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: LOCALIZATED AT FOCAL ADHESION AND CELL-CELL
                                                                                                                                                                                                                                                                                                                                                                                                      Sparks A.B., Hoffman N.G., McConnell S.J., Fowlkes D.M., Kay B.K.;
"Cloning of ligand targets: systematic isolation of SH3 domain-
           OFRIZ8; 062423;
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
VINEXIN (SH3-CONTAINING ADAPTER MOLECULE-1) (SCAM-1) (SH3 DOMAIN-
CONTAINING PROTEIN SH3P3).
                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BINDS TO VINCULIN.
BINDS TO SOS (BY SIMILARITY).
D7716FAID4F0E3CE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00018; SH3; 3.
Pfam; PF02208; Sorb; 1.
PRINTS; PR00452; SH3DOMAIN.
SMART; SM00326; SH3; 3.
SMART; SM00459; Sorb; 1.
PROSITE; PS50002; SH3; 3.
Cytoskeleton; SH3 domain; Repeat; Cell adhesion.
 733 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: CONTAINS 3 SH3 DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGD; MGI:700013; Sh3d4.
InterPro; IPR000108; Neu_cyt_fact_2.
InterPro; IPR001452; SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SORB.
SH3 1.
SH3 2.
SH3 3.
PRT;
                                                                                                                                                                                                                         TISSUE=Embryo;
MEDLINE=99102423; PubMed=9885244;
                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98294438; PubMed=9630982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF064806; AAD32303.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MM.
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 559-733 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              U58889; AAC52642.1; - Q60631; 1GBQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003127; Sorb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82348
 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            579
733
579
733
                                                                                                                               Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            444
674
733 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADHESIONS SITES
                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                              NCBI_TaxID-10090;
                                                                                                            SCAM1 OR SH3D4
                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Embryo;
 VINE_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
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12;

Gaps

37;

91; Indels

6.7%; Score 135.5; DB 15.1%; Pred. No. 0.017; ve 45; Mismatches

25.1%;

Query Match 6.77
Best Local Similarity 25.17
Matches 58; Conservative

DB 1; Length 733;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C2 domain in naryme activity...;
J. Biol. Chem. 273:33082-3309(1998).
-! FUNCTION: PHOSPHORYLATES PTDINS AND PTDINS4P WITH A PREFERENCE FOR PTDINS. DOES NOT PHOSPHORYLATE PTDINS (4,5)P2.
-! CATALYTIC ACTIVITY: ATP + 1-PHOSPHATIDY1-1D-MYO-INOSITOL = ADP + 1-PHOSPHATIDY1-1D-MYO-INOSITOL 3-PHOSPHATE.
-! SUBCELLULAR LOCATION: FOUND MOSTLY IN THE MICROSOME, BUT ALSO IN THE PLASMA MEMBRANE AND CYTOSOL.
-! TRESUE SPECIFICITY: WIDELY EXPRESSED, BUT LEVELS ARE HIGHEST IN THYMUS AND PLACENTA AND LOWEST IN PERIPHERAL BLOOD, SKELETAL MUSCLE AND KIDNEY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: BELONGS TO THE P13/P14-KINASES FAMILY.
-!- SIMILARITY: CONTAINS 1 C2 DOMAIN.
-!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-26 IS THE INITIATOR.
166 NYEKTSGSEMALSTGDVVEVVEKSESGWWFCQMKAKRGWIPASFLEPLDSPDETEDP--E 223
                                                                                                                     573 YVQ----INREPRLRLCDDGPQLPASPNPTTTÄHLSSHS-HPSSIPVDPTDWGGRTSPR 626
                                                                                                                                                                                   275 YLQKSGQDVSQAQR-----QIKRGAPPRRSSIRNAHSIHQRSRKRLSQD----AYR 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arcaro A., Volinia S., Zvelebil M.J., Stein R., Watton S.J.,
Layton M.J., Gout I., Ahmadi K., Downward J., Waterfield M.D.;
"Human phosphoinositide 3-kinase C2beta, the role of calcium and the
                                                                                                                                                                                                                                                                                                                                                                                                                                           PK3B_HUMAN STANDARD; PRT; 1634 AA. 000750; 09566; 20-806-2001 (Rel. 40, Created) 20-806-2001 (Rel. 40, Last sequence update) 20-806-2001 (Rel. 40, Last sequence update) 20-806-2001 (Rel. 40, Last annotation update) PHOSPHATIDYILNOSITIOL 3-KINASE C2 DOMAIN-CONPAINING BETA POLYPEPTIDE (EC 2.71.137) (PHOSPHOINOSITIDE 3-KINASE-C2-BETA) (PT3K-C2BETA) (C2-PI3K).
                           454 DFQAQSPKELSLQKGDIVYIHKEVDKNWLEGEHHGRLGIFPANYVEVLPA-DEIPKPIKP
                                                                                          PNYAGEPYVAIKAYTAVEGD---EVSLLEGEAVEVIHKLLDGWKDD-VT----GYFPSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fry M.J.;
C2 domain-
                                                                                                                                                                                                                                                                                RNSVRF---LQQRRRQARPGPQSPGSPLEEERQTQRSKPQPAVPPRPSADL 369
                                                                                                                                                                                                                                                                                                              MEDLINE-97289668; PubMed-9144573;
Brown R.A., Ho L.K.F., Weber-Hall S.J., Shipley J.M.,
"Identification and cDNA cloning of a novel mammalian
containing phosphoinositide 3-kinase, HSC2-PI3K.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 26-1634 FROM N.A., AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biophys. Res. Commun. 233:537-544(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Monocytes;
MEDLINE=99047700; PubMed=9830063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Y11312; CAA72168.1; -. EMBL; Y13892; CAA74194.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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FODRIN ALPHA CHAIN).
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InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam;
                                                                                                                                    [2]
11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                1367 ISDVFLCRH-----EKIFHPNKGYIYVVKVMRENTHEATYIORTFEEFQELHNKLRLLF 1420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1421 PSS------HLPSFPSRFVIGRSRGEAVAERRREELNGYIWHLIHAPPEVAECD 1468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1529 LOLLQDGNDPDPYVKIYLLPDPQKTTKRKTKVARKTCNPTYNEMLVYD------GIPKG 1581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59 PIEAGAINPENRIIPHLPA-PKWF-----DGQRAAENRQGTLTEYCSTLMSLPTKISRCP 112
                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                             1 MGDTFI-RHIALLGFEKRFVPSQHYVYMFLVKWQDLSEKV-VYRRFTEIYEFHKTLKEMF 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPCN_HUMAN STANDARD; PRT; 2472 AA. 013813; Q16606; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) SPECTRIN ALPHA CHAIN, BRAIN (SPECTRIN, NON-ERYTHROID ALPHA CHAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125 LKLPTDNQTKKP--ETYLMPKDGKST--ATDITGPIILQTYRAIANYEKTSGSEMALSTG
                                                                                                                                                                                                                                                                                                                                                                                                            89;
                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 1634;
                                                                                                                                                                                                                                                                                        75 P > S (IN REF. 2).
75 R > W (IN REF. 2).
76 Q > L (IN REF. 2).
27 W (V > A (IN REF. 2).
27 W (K > E (IN REF. 2).
567 P > S (IN REF. 2).
567 D > S (IN REF. 2).
567 D > S (IN REF. 2).
568 D M > E (IN REF. 2).
568 D M > E (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                           80; Indels
                                                                                                                                                                                                                                                                                                                                                                                        6.6%; Score 133.5; DB 22.1%; Pred. No. 0.068; ive 32; Mismatches
                                                                                                                                                                                         PROSITE; PS00499; C2_DOMAIN_1; FALSE_NEG.
PROSITE; PS0004; C2_DOMAIN_2; FALSE_NEG.
PROSITE; PS00915; PI3_4_KINASE_1; 1.
PROSITE; PS00916; PI3_4_KINASE_2; 1.
PROSITE; PS00290; PI3_4_KINASE_2; 1.
Transferase; Kinase; Multigene family.
                                                                                                                                                                                                                                                                       PI3K/PI4K.
C2 DOMAIN.
                                                                                                                                                                                                                                                       PRO-RICH
                                                                                                                                                                                                                                                               PRO-RICH
                                                      PI3_PI4_kinase
                                    PI3K_ras_bind.
                                                                                           PF00792; PI3K_C2; 1.
PF00794; PI3K_rbd; 1.
PF00454; PI3_PI4_kinase; 1.
                                                                                                                         Pfam; PF00787; PX; 1.
SMART; SM00239; C2; 1.
SMART; SM00145; PI3Ka; 1.
SMART; SM00146; PI3Kc; 1.
SMART; SM00144; PI3K_C2; 1.
SMART; SM00144; PI3K_CB; 1.
                           PI3K_C2.
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| DLQQRELQLSVLSEQGFW 1599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 DV----VEVVEKSESGWW 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         113 HLLDFFKVRPDD------
                                                                                                                                                                                                                                                                                                                                                                                        Query Match 6.6
Best Local Similarity 22.1
Matches 57; Conservative
                                                                                    PF00613; PI3Ka; 1.
                                                                                                                                                                                                                                                                                                   75
246
278
567
665
                                                                          PF00168; C2; 1.
                  InterPro; IPR000008;
                           InterPro; IPR002420;
InterPro; IPR000341;
                                             InterPro; IPR001263;
                                                        InterPro; IPR000403;
                                                                 InterPro; IPR001683;
                                                                                                                                                                                                                                                                                                                                                           1634 AA;
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                                                                                                                                                                                                                                                                         DOMAIN
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                                                                                             Pfam;
                                                                                                       Pfam;
Pfam;
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SPCN_HUMAN
ID SPCN_H
AC 013813
DT 01-NOV
DT 20-AUG
DE SPECTR
                                                                            Pfam;
                                                                                    Pfam;
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                                                                                                                                                                                                                                                                                                                                                  polypeptides are predicted by sequence analysis of cDNAs encompassing
the coding region of human nonerythroid alpha-spectrin.";
J. Biol. Chem. 265:4427-4433(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [3] SEQUENCE OF 676-1595 FROM N.A. SEQUENCE OF 676-1595 FROM N.A. MEDLINE-87277023; PubMed=3038643; McMahon A.P., Giebelhaus D.H., Champion J.E., Bailes J.A., Lacey S., Carritt B., Henchman S.K., Moon R.T.; "cDNA cloning, sequencing and chromosome mapping of a non-erythroid spectrin, human alpha-fodrin."; Differentiation 34:68-78(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN: SPECTRIN-LIKE PROTEINS HAVE FIVE DOMAINS:

(2) DOMAIN BETWEEN THE N-TERMINAL AND MIDDLE DOMAIN (NM),

(3) MIDDLE DOMAIN (M),

(4) DOMAIN BETWEEN THE MIDDLE AND C-TERMINAL DOMAIN (MC),

(5) C-TERMINAL DOMAIN (C),

NM AND MC DOMAINS ARE COMPOSED OF TYPICAL SPECTRIN 106 RESIDUES

NEEPERTS (1-8 FOR NM AND 12-19 FOR MC) AND ARE HOMOLGGOUS TO EACH

OTHER, N, M, AND C DOMAINS ARE COMPOSED OF SEQUENCES THAT DO NOT

PORM TYPICAL SPECTRIN REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MCMAIND. A.P., Glebelhaus D.H., Champion J.E., Bailes J.A., Lacey S., Carritt B., Henchman S.K., Moon R.T.;
Differentiation 34:241-241(1987).
-!- FUNCTION: FODRIN, WHICH SEEMS TO BE INVOLVED IN SECRETION, INTERACTS WITH CALMODULIN IN A CALCIUM-DEPENDENT MANNER AND IS THUS CANDIDATE FOR THE CALCIUM-DEPENDENT MOVEMENT OF THE CYTOSKELETON AT THE MEMBRANE.
-!- SUBJUNIT: LIKE BRYTHROCYTE SPECTRIN, THE SPECTRIN-LIKE PROTEINS ARE CAPABLE TO FORM DIMBERS WHICH CAN FURTHER ASSOCIATE TO
                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                Generation of diversity in nonerythroid spectrins. Multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       McMahon A.P., Moon R.T.;
"Structure and evolution of a non-erythroid spectrin,
alpha-fodrin.";
Biochem. Soc. Trans. 15:804-807(1987).
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                                                                                                                                                                                                                                                 MEDLINE=90170948; PubMed=2307671;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IISSUE=Lung;
MEDLINE=88083942; PubMed=3691949;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 676-1595 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR001452; SH3.
IPR002017; Spectrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; J05243; AAA51790.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M24773; AAA52468.1;
EMBL; M18627; AAA51702.1;
HSSP; P07751; 1AEY.
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                                                                                                                                                                                                                                                                                      Moon R.T., McMahon A.P
                                                                                                                                                                           [1]
SEQUENCE FROM N.A.
                                                                                                                                             NCBI_TaxID=9606;
SPTAN1 OR SPTA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TETRAMERS.
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SEQUENCE FROM N.A.
                           NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Spleen
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                                                                                                                                                                                                                                                                              DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                 Best Local
                                                                          gene.";
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  969 K--------ELVLALY----DYQEKSPREVTMKKGDILTLINSTNKDWW 1005
                                                                                                                                                                                                                                                                                                                                                                                          923 ---DSAEALLKKHEALMSDLSAYGSSIQALREQAQSCRQQV------APTDDETG 968
                                                                                                                                                                                                                                                                                                                                                                                 195 FCQMKAKRGWIPASFLEPLDSPDETEDPEPNYAGEPYVAIK-----AYTAVEGDEVSL 247
                                                                                                                                                                                                                                                                                                                                                       135 KPETYLMPKDGKSTATDITGPIILQTYRAIANYEKTSGSEMALSTGDVVEVVEKSESGWW 194
                                                                                                                                                                                                                                                                                                                             79 KWFDGQRAA----ENRQGTLTEYCSTLMSLPTKISRCPHLLDFFKVRPDDLKLPTDNQTK 134
                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                   31 KWQDLSEKVVYRR-----FTEIYEFHKTLKEMFPIEAGAINPENRIIPHLPAP 78
                                                                                                                                                                                                                                                                                                               871 KWEALKAKASQRRQDLEDSLQAQQYFADANEAESWMREKEPIVGSTDYGKDE-----
                                                                                                                                                                                                                                                                                     :69
                                                                                                                                                                                                                                                                        DB 1; Length 2472;
                                                                                                                                                                                                                                                                       6.6%; Score 133.5; DB 1; Length
19.3%; Pred. No. 0.12;
ive 45; Mismatches 91; Indels
                                                                                                                                                                                                                               EF-HAND 1 (POTENTIAL).
EF-HAND 2 (POTENTIAL).
F -> R (IN REF. 2 AND 3).
W; CDA1964462A7028D CRC64;
                                                                                                                                                11.
12.
12.
14.
15.
16.
17.
19.
20.
21.
C-TERMINAL DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
04-AGG-2001 (Rel. 40, Last annotation update)
CRK-LIKE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           303 AA
                                                                                                                             MIDDLE DOMAIN. SH3.
                                                                                                                                          DOMAIN
Pfam; PF00435; spectrin; 23.
PRINTS; PR00452; SH3DOMAIN.
                                                                                                                                                                                                                                                    2472 AA; 284279
                                                                                                                                                                                                                                                                        Query Match 6.6
Best Local Similarity 19.3
Matches 49; Conservative
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the European Bioinformatics Institute. There are no restrictions on
use by non-profit institutions as long as its content is in no
modified and this statement is not removed. Usage by and for commer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 LVRSSPHGKHGNRNSNSYGIPEPAHAYAQPQTTTPLPAVSGSPGAAITPLPSTQNGPVFA 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61; Gaps
                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                          MEDIINE=53368949; PubMed-8361759;
ten Hoeve J., Morris C., Heisterkamp N., Groffen J.;
"Isolation and chromosomal localization of CRKL, a human crk-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 303;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----SLLEGEAVEVIHKLLDG-WKDDVT---GYFPSMYLQ 277
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SH3 2.
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PRINTS; PRO0461; SH3DOMAIN.
SMART; SM00252; SH2: 1.
SMART; SM00326; SH3: 2.
PROSITE; PS50001; SH2: 1.
PROSITE; PS50001; SH3: 1.
SH2 domain; SH3 domain.
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InterPro; IPR000980; SH2.
InterPro; IPR00145; SH3.
Pfam; PF00017; SH2; 1.
Pfam; PF00018; SH3; 1.
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RA Adams M.D., Celnis Furbact-10/3113;

RA Adams M.D., Celnis Furbact S.E., Li P.W., Hoskins R.A., Galle R.E.,

RA Adams M.D., Celnis Furbacts S.E., Li P.W., Hoskins R.A., Galle R.E.,

RA George B. G., Scherz S.E., Li P.W., Hoskins R.A., Galle R.E.,

Sutton G.G., Wortman J.E., Flichards S., Ashburner M. L.X.,

RA Braddon R.C., Rogers Y.-H.C., Blazej R.G., Change M., Picfelfer B.D.,

RA Adams M.D., Celnis Baren E.G., Helt G., Nalson C.R., Mikhos G.L.G.,

RA Adams M.D., Baxen R.A. Blazej R.G., Change M., Picfelfer B.D.,

RA Ballew R.W., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Ballew R.W., Basu A., Baxendale J., Bayraktaroglu L., Baldakov S.,

Ballew R.W., Bauch M.R., Bouck J., Bayraktaroglu L., Baldakov S.,

Ballew R.W., Cawley S., Dahlke C., Davemport L.B., Davies P.,

RA Burtis R.C., Busam D.A., Buller H., Cadleu E., Center A., Chadra I.,

RA Cawley S., Dahlke C., Davemport L.B., Davies P.,

RA Burtis R.C., Busam D.A., Buller H., Cadleu E., Center A., Dunn P.,

RA Dodson R., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Burtis R.C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gaun P., Harris M.,

RA Hostin D., Houston K.A., Helman T.J., Well M.-H., Ibeywam C.,

Alalbi M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Alalbi M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Balzzolo M., Pittman G.S., Pan S., Pollard J., Purl V., Reese M.G.,

RA Shue B.C., Stadelier R., Wonders Y. Owners C., Wang S., Nan B.,

Syler E., Spradling A.C., Stapleton M., Skupski M.P., Smith H.O.,

Mullams S.M., Woodang T., Wonders C., Wang S., Nan G.,

RA Wang Z.-Y. Wassarman D.A., Wellsten B., Shan G.,

Sheng X.H., Zhong F.N., Zhong W., Zhou X., Zha S., Zha O., Zha O.
SPECTRIN ALPHA CHAIN.
ALPHA-SPEC OR SPEC-A OR CG1977.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryyota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHARACTERIZATION.
MEDLINE-88059242; PubMed-3680372;
Dubreuil R., Byers T.J., Branton D., Goldstein L.S.B., Kiehart D.P.;
"Drosophilia spectrin. I. Characterization of the purified protein.";
J. Cell Biol. 105:2095-2102(1987).
                                                                                                                                                                                                                                                                                                 "The complete sequence of Drosophila alpha-spectrin: conservation of structural domains between alpha-spectrins and alpha-actinin."; J. Cell Biol. 109:2197-2205(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-150 AND 2192-2415 FROM N.A., AND CHARACTERIZATION. MEDLINE=94103334; Pubmed=8276898;
                                                                                                                                                                                                                                                 Dubreuil R.R., Byers T.J., Sillman A.L., Bar-Zvi D., Goldstein L.S.B., Branton D.; The complete sequence of Drosophila alpha-spectrin:
                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-20196006; PubMed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster.";
J. Cell Biol. 123:1797-1809(1993).
                                                                                                                                                                                                                                MEDLINE=90037215; PubMed=2808524;
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MEDLINE-89234159; PubMed=2497103;

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THE IT, MINDIGHAE TO THE TOTAL HOLD HOLD SEARCH STANDER TO THE TOTAL THE TOTAL TOTAL HOLD SEARCH STANDER TO THE CYTOSKELETAL SCIENCE 262:2027-2030(1993).

SCIENCE 262:2027-2030(1993).

POSTINE SECTRIN IS THE MAJOR CONSTITUENT OF THE CYTOSKELETAL METHORY BE LEAST METHORY TO THE ERYTHROCYTE PLASMA MEMBRANE. IT ASSOCIATES WITH BAND 4.1 AND ACTIN TO FORM THE CYTOSKELETAL SUPERSTRUCTURE OF THE ERYTHROCYTE PLASMA MEMBRANE. ESSENTIAL FOR LARVAL SURVIVAL AND DEVELOPMENT. STABILIZES CELL TO CELL INTERACTIONS THAT ARE CRITICAL FOR THE MAINTENANCE OF CELL SHAPE AND SUBCELLULAR ORGANIZATION WITHIN EMBRYONIC TISSUES.

C. I. SUBUNIT. NATIVE SPECTRIN MOLECULE IS A TETRAMER COMPOSED OF TWO ANTIPRAALLEL HETERODIMERS JOINED HEAD TO HEAD SO THAT EACH END OF THE NATIVE MOLECULE INCLUDES THE C-TERMINGS OF THE ALPHA SUBUNIT. INTERACTS WITH CALMODULIN IN A CALCIUM-DEPENDENT MANNER AND INTERACTS WITH F-ACTIN.

SUBCELLULAR LOCATION. NEAR THE INNER SURFACE OF THE PLASMA MEMBRANE OF NEARLY ALL CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                between the Swiss Institute of Bioinformatics and the EMBL outstation —
the Buropean Bioinformatics Institute. There are no restrictions on its
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modified and this statement is not removed. Usage by and for commercial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE SPECIFICITY: A SUBSTANTIAL POOL OF MATERNAL PROTEIN IN THE BGG UNDERGOES DYNAMIC CHANGES IN DISTRIBUTION EARLY IN EMBRYOGENESIS. IN GASTRULATED EMBRYO, THE HIGHEST LEVEL OF PROTEIN IS FOUND IN THE RESPIRATORY TRACT CELLS AND THE LOWEST IN PARTS OF THE FORMING GUT.
Pesacreta T.C., Byers T.J., Dubreuil R., Kiehart D.P., Branton D.; "Drosophila spectrin: the membrane skeleton during embryogenesis."; J. Cell Biol. 108:1697-1709(1989).
                                                                                                                         Yan Y., Winograd E., Viel A., Cronin T., Harrison S.C., Branton D.,
"Crystal structure of the repetitive segments of spectrin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -:- DEVELOPMENTAL STAGE: EXPRESSED BOTH MATERNALLY AND ZYGOTICALLY.
-:- SIMILARITY: BELDONGS TO THE SPECTRIN FAMILY.
-:- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
-:- SIMILARITY: CONTAINS 22 SPECTRIN REPEÄTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cytoskeleton; Membrane; Erythrocyte; Repeat; Actin-binding; Capping protein; Calcium-binding; SH3 domain; 3D-structure;
                                                                                 x-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 1391-1497
MEDLINE=94090340; PubMed=8266097;
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SPECTRIN 7
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SPECTRIN 9
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SPECTRIN 9
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EMBL; AE003472; AAF47569.1; -
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SMART; SM00054; EFh; 2.
SMART; SM00326; SH3; 1.
SMART; SM00150; SPEC; 20.
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Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----YFPSMYLQKSGQDVSQAQRQIKRGAPPRRSSIRNAHSI 307
                                                                                                                                                                                                                                                                                                                                           79 KWFDGQRAAENRQGTLTE----YCSTLMSLPTKISRCPHLLDFFKVRPDDLKLPTDNQTK 134
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Last annotation update)
BRAIN (SPECTRIN, NON-ERYTHROID ALPHA CHAIN)
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                                                                                                                                                                                                                                             DB 1; Length 2415;
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MEDLINE-89093238; PubMed-2910879;
Wasenius V.-M., Saraste M., Salven P., Eraemaa M., Holm M.,
                                                                                                                                                                               -> D (IN REF. 3).
-> R (IN REF. 1).
F1F72FB990EB0A37 CRC64;
                                                                                                                                           EF-HAND 1 (POTENTIAL).
EF-HAND 2 (POTENTIAL).
SH3.
Q -> D (IN REF. 3).
Q -> R (IN REF. 1).
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                                                                                                                                                                                                                                                                    62; Mismatches 114;
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                                                                                                                                                                                                                                            Score 131.5; D
Pred. No. 0.16;
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                                                                                  SPECTRIN 18.
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SPECTRIN 22
            SPECTRIN 3
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01-AUG-1991 (Rel. 19, Last seq
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Best Local Similarity 15.3'
Matches 56; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPCN_CHICK
P07751;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         268 TG--
                                                                                                                                                                                            CONFLICT
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CA_BIND
CA_BIND
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This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 969-1025.
MEDLINE-9833217; Pubmed-9699637;
Martinez J.C., Pisabarro M.T., Serrano L.;
"Obligatory steps in protein folding and the conformational diversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=96067121; PubMed=7588621;
Trave G., Lacombe J.-P., Pfuhl M., Saraste M., Pastore A.;
"Molecular mechanism of the calcium-induced conformational change in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REPEATS (1-8 FOR NM AND 12-19 FOR MC) AND ARE HOMOLOGOUS TO EACH OTHER. N, M, AND C DOMAINS ARE COMPOSED OF SEQUENCES THAT DO NOT FORM TYPICAL SPECTRIN REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (5) C-TERMINAL DOMAIN (C).
NM AND MC DOMAINS ARE COMPOSED OF TYPICAL SPECTRIN 106 RESIDUES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBO J. 14:4922-4931(1995).

EMBO J. 14:4922-4931(1995).

PERATED TO SPECTRIN, SPECTRIN-LIKE PROTEINS APPEAR TO BE RELATED TO SPECTRIN, SHOWING A FLEXIBLE ROD-LIKE STRUCTURE. THEY CAN BIND ACTIN BUT SEEM TO DIFFER IN THEIR CALMODULINBINDIA ACTIN BUT SEEM TO DIFFER IN THEIR CALMODULINBINDIA ACSOCIATION WITH SOME OTHER PROTEINS, MAY PLAY AN IMPORTANT ROLE IN MEMBRANE ORGANIZATION.

POLE IN MEMBRANE ORGANIZATION.

PERRAMERS.

PERRAMERS.
                                                                                                                                                                  SEQUENCE OF 1695-2153 FROM N.A. MEDLINE-89284928; PubMed-4029118; Masorius V.-M., Saraste M., Knowles J., Virtanen I., Lehto V.-P.; Masorius V.-M., Saraste M., Knowles J., Virtanen I., Lehto V.-P.; "Sequencing of the chicken non-erythroid spectrin cDNA reveals an internal repetitive structure homologous to the human erythrocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (1) N-TERMINAL DOMAIN (N), (2) DOMAIN BETWEEN THE N-TERMINAL AND MIDDLE DOMAIN (NM),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MIDDLE DOMAIN (M), DOMAIN BETWEEN THE MIDDLE AND C-TERMINAL DOMAIN (MC),
                                                                                                                                                                                                                                                                                                                                                                               Musacchio A., Noble M., Pauptit R., Wierenga R., Saraste M.; "Crystal structure of a Src-homology 3 (SH3) domain."; Nature 359:851-855(1992).
                                                                                   Eraemaa M., Holm L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDILINE-38022917: PubMed-9356261;
Pascual J., Pfuhl M., Walther D., Saraste M., Nilges M.;
Solution structure of the spectrin repeat: a left-handed antiparallel triple-helical coiled-coil.";
J. Mol. Biol. 273:740-751(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN: SPECTRIN-LIKE PROTEINS HAVE FIVE DOMAINS:
                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 965-1025.
MEDLINE=93063299; PubMed=1279434;
"Primary structure of the brain alpha-spectrin.";
J. Cell Biol. 108:79-93(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE SPECTRIN FAMILY. SIMILARITY: CONTAINS 1 SH3 DOMAIN.
                                                                                 Wasenius V.-M., Saraste M., Salven P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Struct. Biol. 5:721-729(1998)
                                                                                                     Lehto V.-P.;
J. Cell Biol. 108:1177-1178(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRUCTURE BY NMR OF 1763-1872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRUCTURE BY NMR OF 2320-2403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the transition state.";
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                                                               REVISIONS.
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79 KWFDGQRAA----ENRQGTLTEYCSTLMSLPTKISRCPHLLDFFKVRPDDLKLPTDNQTK 134
                                       g
                                                       Óγ
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rub; 1SHG; 31-OCT-93.

PDB; 1ABY; 15-MAY-97.

DR PDB; 1ABY; 15-MAY-97.

DR PDB; 1ABY; 15-MAY-97.

DR PDB; 1AJ3; 07-JUL-97.

DR PDB; 1TUD; 01-AUG-96.

DR PDB; 1EK2; 16-FEB-96.

DR InterPro; 1PR001461; EF-hand.

DR InterPro; 1PR001461; SH3.

DR Ffam; PF00036; efhand; 2.

DR PFAm; PF00036; efhand; 2.

DR PFAm; PR001452; SH3.

DR PRINTS; PR00452; SH3.

DR SWART; SW00364; EFH; 2.

DR SWART; SW00364; EFH; 2.

DR SWART; SW00169; SFEC; 20.

DR PROSITE; PS00018; EH3: 1.

DR ROSITE; PS00018; EH3: 1.

ET REPEAT 120 Calmodulin-binding; Actin-binding; KW Cytoskeleton; Membrane; Calmodulin-binding; Duplication; Repeat; SH3 domain; KW SPEAT 120 225 2.

FT REPEAT 120 225 2.

FT REPEAT 120 225 2.

FT REPEAT 120 225 2.
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MC DOMAIN.
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SEQUENCE
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CA_BIND
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                                                      -----ELVLALY----DYQEKSPREVTMKKGDILTLLNSTNKDWW 1005
                                                                                                  195 FCQMKAKRGWIPASFLEPLDSPDETEDPEPNYAGEPYVAIK-----AYTAVEGDEVSL 247
---DSAEALLKKHEALMSDLSAYGSSIQALREQAQSCRQQV-----APTDDETG 968
                           135 KPETYLMPKDGKSTATDITGPIILQTYRAIANYEKTSGSEMALSTGDVVEVVEKSESGWW 194
                                                                                                                                                                                                                                                                                                                                          Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SH2.
SH3 1.
SH3 2.
; B8126DDFF2053573 CRC64;
                                                                                                                                                                                                                                                          01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
CRK_LIKE PROTEIN.
CRKL OR CRKOL.
                                                                                                                                                                                                                                     303 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00255; SH2; 1.
SWART; SM00255; SH2; 1.
SNART; SM00156; SH3; 2.
PROSITE; PS50001; SH2; 1.
PROSITE; PS50002; SH3; 1.
SH2 domain; SH3 domain; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=C57BL X CBA; TISSUE=Placenta;
                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=96038874; PubMed=7478571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33817 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:104686; Crkol.
InterPro; IPR000980; SH2.
InterPro; IPR001452; SH3.
Pfam; PF00017; SH2: I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00401; SH2DOMAIN.
PRINTS; PR00452; SH3DOMAIN.
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1065 RMKQVEELYHSLLE 1078
                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                     248 LEGEAVEVIHKLLD 261
                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
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123
235
303 AA;
                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                     CRKL_MOUSE
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DOMAIN
DOMAIN
SEQUENCE
                                                      Ÿ.
                                                                                                                                                                                                                     CRKL_MOUSE
923
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8

Length 2477; Indels

DB 1;

6.5%; Score 131.5; DB 19.3%; Pred. No. 0.16; tive 44; Mismatches

Conservative

Matches

31

ò qQ

Query Match Best Local Similarity 49;

871 KWDSLKAKASQRRQDLEDSLQAQQYFADANEAQSWMREKEPIVGSTDYGKDE----- 922 KWQDLSEKVVYRR-------FTEIYEFHKTLKEMFPIEAGAINPENRIIPHLPAP 78

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                                                                                                                              LVRSSPHGKHGNRNSNSYGIPEPAHAYAQPQTTTPLPTVASTPGAAINPLPSTQNGPVFA 240
                                                        103 SLPTK-----ISRCPHLLDFFKVRPDDLKLPTDNQTKRPETYLMPKDGKSTATDI-T 153
                                                                                  65 SLPNRRFKIGDQEFDHLPALLEFYKIH----YLDTTTLIEPAPRYPSPPVGSVSAPNLPT 120
                                                                                                           154 GPIILQTYRAIANYEKTSGSEMALSTGDVVEVVEKSESGWWFCQMKAKR-GWIPASFLEP 212
                               Gaps
                                                                                                                                                                                                                                                                                                                    FGR_MOUSE STANDARD; PRT; 517 AA.
P14234: Q61404;
01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PROTO-ONCOGENE TYROSINE-PROTEIN KINASE FGR (EC 2.7.1.112) (P55-FGR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Cloning of the murine c-fgr proto-oncogene cDNA and induction of c-fgr expression by proliferation and activation factors in normal bone marrow-derived monocytic cells."; oncogene 4:10811087(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  King F.J., Cole M.D.;
"Molecular cloning and sequencing of the murine c-fgr gene.";
"moscene S:337-344(1990).
-!- CATALYTIC ACTIVITY: AFP + A PROFEIN TYROSINE - ADP +
PROTEIN TYROSINE PHOSPHATE.
-!- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
-!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
-!- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
DOMAIN. BELONGS TO THE SRC SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae; Mus
                              61;
                                                                                                                                                                                                                       ---SLLEGEAVEVIHKLLDG-WKDDVT---GYFPSMYLQ 277
                                                                                                                                                                                                                                       241 KAIQKRVPCAYDKTALALEVGDIVKVTRMNINGQWEGEVNGRKGLFPFTHVK 292
 Length 303;
                              Indels
                            86;
  DB 1;
6.4%; Score 129.5; DB 21.6%; Pred. No. 0.015; Live 35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE-Monocytic leukemia;
MEDLINE-90191719; PubMed-2179817;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=DBA/2J;
MEDLINE=89385605; PubMed=2674853;
Yi T.L., Willman C.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP, P00523; 2PTK.
MGD; MGI:95527; Fgr.
InterPro; IPR000719; Euk_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X16440; CAA34463.1; -. EMBL; X52191; CAA36437.1; -.
                            50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A33127; A33127.
PIR; S10072; S10072.
HSSP; P00523; 2PTK.
  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                       (C-FGR).
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                            Matches
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SH2.
PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68 TIFVALYDYEARTGDDLTFTKGEKFHILNNTEYDWWEARSLSSGHRGYVPSNYVAPVDSI 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   217 DETE-----DPEPNY--AGEPY------VAIKAYTAVEGDEVSLLE 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          250 GEAVEVIHKLLDGWKDDVTGYFPSMYLQ-KSGQDVSQAQRQIKRG-----APPRRSSIR 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       303 NAHSIHQRSRKRLSQDAYR--RNSVRFLQQRR-------------RQARPG 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transferase; Tyrosine-protein kinase; Proto-oncogene; ATP-binding;
Phosphorylation; SH2 domain; SH3 domain.
DOMAIN 65 126 SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       161 --YRAIANYEKTSGSEMALSTGDVVEVVEKSESGWWFCQ--MKAKRGWIPASFLEPLDSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                236 TL------GLAKDAWEIDRNSIAL--ERRLGTGCFGDVWLGTWNCSTKVAVKTLKPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 129.5; DB 1; Length 517; Pred. No. 0.029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F655BDB4510F3076 CRC64;
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Q -> R (IN REF. 2)
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21.0%; Pred. No. v..
                                                                                               PRINTS; PRO0109; TYRKINASE.
PRINTS; PR00109; TYRKINASE.
PRINTS; PR00401; SH2DOMAIN.
SMART; SM00252; SH3DOMAIN.
SMART; SM00326; SH3; 1.
SMART; SM00319; TYRKC; I.
PROSITE; PS00109; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.
PROSITE; PS50011; SH2; 1.
PROSITE; PS50011; SH2; 1.
InterPro; IPR001452; SH3.
InterPro; IPR001245; Tyr_kin.
Pfam; PP000019; Pkinase; 1.
Pfam; PF00017; SH2; 1.
Pfam; PF00018; SH3; 1.
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517 AA;
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285 TMSPKAFLEE 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
nes 65; Conserv
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MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
```

16;

Search completed: January 11, 2002, 09:11:26 Job time: 208 sec

r .

Gencore version 4.5 (c) 1993 - 2000 Compugen Ltd. Copyright

OM protein – protein search, using sw model

January 11, 2002, 09:05:54 ; Search time 15.91 Seconds (without alignments) 1848.107 Million cell updates/sec Run on:

US-09-820-005-2 2035 1 MGDTFIRHIALLGFEKRFVP......ADLILNRCSESTKRKLASAV 386 score: Perfect so Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

219241 seqs, 76174552 residues

Searched:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

PIR_68:* Database :

1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ID	Description
	2018	99.2	390	-	A39249	neutrophil cytosol
7	1666	81.9	388	7	I54525	Ψ
٣	275	13.5	940	7	T00056	hypothetical prote
4	179.5	8.8	1270	7	T09194	adaptor protein in
S	169.5	8.3	339	7	S39768	neutrophil cytosol
9	164.5	8.1	639	7	T13151	adapter protein CM
7	164	8.1	1011	7	T13055	
œ	161	7.9	1094	7	T13053	
6	150.5	7.4	665	7	JC7191	85K c-Cbl-interact
10	147.5	7.2	290	~	T42526	hypothetical prote
11	145	7.1	1119	~1	T50995	related to cytoske
12	142.5		1097	N	T31504	hypothetical prote
13	139	9.9	443	7	T27877	
14	136	6.7	50	4	A58224	$\rightarrow$
15	135.5	6.7	816	7	T17257	hypothetical prote
16	133.5		1634	٦	JC5500	u
17	133.5	9.9	2472	7	A35715	fodrin alpha chain
18	133	-:	408	7	T26940	hypothetical prote
19	131.5		303	~	S41754	
20	131.5	6.5	2415	Н	A33733	spectrin alpha cha
21	131.5		2477	-	SJCHA	spectrin alpha cha
22	130.5	6.4	1196	~	T14108	
23	129.5	6.4	303	7	S58352	М
24	127.5	6.3	505	-	S24550 ·	w
25	127.5	6.3	1249	7	A56511	myosin I myoA - Em
26	127	6.2	1244	7	S25327	cytoskeleton assem
27	125.5	6.2	517	7	A43807	>
28	125.5	6.2	1109	7	S53601	myosin-IC [similar
29	124	6.1	305	Н	A49011	

probable myosin I hypothetical prote	myosin I heavy cha	myosin heavy chain	uvs2 protein - Neu	scd2 protein - fis	hypothetical DAG-b	hypothetical prote	hypothetical prote	neutrophil oxidase	neuron-specific si	hypothetical prote	phosphoinositide 3	hypothetical prote	SH3 domains-contai	myosin heavy chain
T39427 T33339	S52517	MWAXIB	S34825	T38210	T39376	T26607	T16613	S27788	JC5269	T42650	T42642	T46356	T09071	A47106
(4 (4		ī	(A	7	(4	7	7	7	7	7	7	7	~	7
1217 2	1107 1	1147 1	501 2	536 2	642 2	728 2	2427 2	359 2	403 2	408 2	1658 2	496 2	892 2	1113 1
6.1 1217 2 6.1 648 2	6.0 1107 1	6.0 1147 1	6.0 501 2	5.9 536 2	5.9 642 2	5.9 728 2	5.9 2427 2	5.9 359 2	5.9 403 2	5.8 408 2	5.8 1658 2	5.7 496 2	5.7 892 2	5.7 1113 1
124 6.1 1217 2 123.5 6.1 648 2	6.0	0.9	0.9	5.9	ري 6.	5.9	5.9	5.9	6.5	5.8	9.0	5.7	5.7	5.7

## ALIGNMENTS

neutrophil cytosol factor 1 - human
N;Alternate names: 47K autosomal chronic granulomatous disease protein; multicomponen
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 18-Jun-1999
C;Accession: A35926; A39249; A34067; I59199; A32762; A41365
R;Rodaway, A.R.F.; Teahan, C.G.; Casimir, C.M.; Segal, A.W.; Bentley, D.L.
Mol. Cell. Biol. 10, 5388-5396, 1990
A;Title: Characterization of the 47-kilodalton autosomal chronic granulomatous diseas
A;Reference number: A35926
A;Reference number: A35926

A; Molecule type: mRNA A; Residues: 1-390 <ROD> A;Cross-references: GB:M35067; GB:M38755; NID:g189050; PIDN:AAA59901.1; PID:g189051 R;Volpp, B.D.; Nauseef, W.M.; Donelson, J.E.; Moser, D.R.; Clark, R.A. Proc. Natl. Acad. Sci. U.S.A. 86, 9563, 1989 A; Reference number: A39249

A; Contents: erratum A; Accession: A39249

A; Residues: 1-390 <VOL.
A; Residues: 1-390 <VOL.
A; Residues: 1-390 <VOL.
A; Residues: 1-390 <VOL.
A; Cross-references: GB:N25665; GB:N26193; NID:g189107; PIDN:AA57209.1; PID:g189108
A; Cross-references: GB:N2665; GB:N26193; NID:g189107; PIDN:AA57209.1; PID:g189108
A; Title: Cloning of the cDNA and functional expression of the 47-kilodalton cytosolic
A; Reference number: A41385; MUID:89386707
A; Reference number: A41385; MUID:89386707
A; Note: the sequence reported has been extensively revised in reference A39249
A; Title: Recombinant 47-kilodalton cytosol factor restores NADPH oxidase in chronic g
A; Reference number: A32762; MUID:89332501
A; Contents: annotation
A; Note: the sequence reported has been extensively revised and now agrees with that s
A; Contents: annotation
A; Note: the sequence reported has been extensively revised and now agrees with that s
A; Finan, P; Shimizu, Y; Gout, I; Hsuan, J; Truong, O; Butcher, C; Bennett, P;
J; Biol. Chem. 269, 13752.13752, 1994
A; Title: An SH3 domain and proline-rich sequence mediate an interaction between two c
A; Reference number: A54067; MUID:94245680
A; Accession: A54067

A; Molecule type: protein
A; Residues: 8-16;44-52;71-77 <FIN>
A; Residues: 8-16;44-52;71-77 <FIN>
A; Residues: 8-16;44-52;71-77 <FIN>
B; Casimir, C.M.; Bu-Ghanim, H.N.; Rodaway, A.R.F.; Bentley, D.L.; Rowe, P.; Segal, A. Proc. Natl. Acad. Sci. U.S.A. 88, 2753-2757, 1991
A; Title: A tucsomal recessive chronic granulomatous disease caused by deletion at a dial A; Reference number: 159190; MUID:91187870

A;Status: translated from GB/EMBL/DDBJ A;Molecule type: DNA

A;Residues: 14-24 <CAS> A;Cross-references: GB:M60941; NID:g189948; PIDN:AAA60086.1; PID:g189949

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DTFIRHIALLGFEKRFIPSQHYVYMFLVKWQDLSEKVVYRKFTEIYEFHKMLKEMFPIEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <ISH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-940 <ISI
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        residue
A,Note: a GT dinucleotide deletion at a GT-GT repeat causes a frameshift after residue C;Comment: This protein is required for activation of the latent NADPH oxidase, which cous disease.

C;Genetics:
A;Gene: GDB:NCF1
A;Cross-references: GDB:120222; OMIM:233700
A;Map position: 7q11.23-7q11.23
A;Note: the list of introns is incomplete
C;Superfamily: neutrophil cytosol factor 1; SH3 homology
C;Keywords: cytosol; neutrophil cytosol factor 1; SH3 homology
F;163-210/Domain: SH3 homology <SH31>
F;233-280/Domain: SH3 homology <SH32>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             leukemia-related protein - mouse (fragment)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Species: O2-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 16-Jul-1999
C; Accession: 154525
R; Jackson, S.H.; Malech, H.L.; Kozak, C.A.; Lomax, K.J.; Gallin, J.I.; Holland, Simunogenetics 39, 272-275, 1994
A; Title: Cloning and functional expression of the mouse homologue of p47phox.
A; Reference number: 154525
A; Accession: 154525
A; Accession: 154525
A; Mulb: 94164697
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-388 cRES-
A; Cross-references: GB:L11455; NID:3309422; PIDN:AAA50469.1; PID:g557868
C; Superfamily: neutrophil cytosol factor 1; SH3 homology
F; 161-208/Domain: SH3 homology <SH31>
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                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                  1 MGDTFIRHIALLGFEKRFVPSQHYVYMFLVKWQDLSEKVVYRRFTEIYEFHKTLKEMFPI
                                                                                                                                                                                                                                                                                                                                                                                                                         RPDDLKLPTDNQTKKPETYLMPKDGKSTATDITGPIILQTYRAIANYEKTSGSEMALSTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EGDEVSLLEGEAVEVIHKLLDGW----KDDVTGYFPSMYLQKSGQDVSQAQRQIKRGAPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RRSSIRNAHSIHQRSRKRLSQDAYRRNSVRFLQQRRRQARPGPQSPGSPLEEERQTQRSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DVVEVVEKSESGWWFCQMKAKRGWIPASFLEPLDSPDETEDPEPNYAGEPYVAIKAYTAV
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9
                                                                                                                                                                                                                                        Length 390;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81.9%; Score 1666; DB 2;
80.2%; Pred. No. 5.7e-119;
ive 35; Mismatches 36;
                                                                                                                                                                                                                                      Score 2018; DB 1;
Pred. No. 1.1e-145;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PQPAVPPRPSADLILNRCSESTKRKLASAV 386
                                                                                                                                                                                                                                      99.2%;
llarity 98.7%;
Conservative
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Best Local Similarity
Matches 385; Conserv
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nes 312; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Accession: T00056
R; Ishikawa, K; Nagase, T; Nakajima, D.; Sekl, N.; Ohira, M.; Miyajima, N.;
submitted to the EMBL Data Library, October 1997
A; Description: Prediction of the coding sequences of unidentified human genes
A; Reference number: 214080
A; Accession: T00056
A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein KIAA0418 - human
C;Species: Homo sapiens (man)
C;Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 05-Nov-1999
                                                                                                                                                                                         242
                                                                                                                                                                                                               --GWAPASYLKKAKDDLPTRKKNLAGPVEIIGNIMEISNLLNKKASGDKETPPAEGEGHE 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APIAKKEISLPILCNASNGSAVGVPDRTVSRLAQGS--PAVARIAPQRAQISSPNLRTRP 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                     DEVSLLEGEAVEVIHKLLDGW----KDDVTGYFPSMYLQKSGQDVSQAQRQIK-RGAPPR
                                                                                                                                                                                                                                                                                                                                                                                    RSSIRNAHSIHQRSRKRLSQDAYRRNSVRFLQQRRRQARPGPQSPGSPLEEERQTQRSKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  156 IILQTYRAIANYEKTSGSEMALSTGDVVEVVEKSESGWWFCQMKAKRGWIPASFLEPLDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---RSSIRNAHSIHQRSRKRLSQDAYRRNSVRFLQQRRRQARPGPQSPG
GAINPENRIIPHLPAPKWFDGQRAAENRQGTLTEYCSTLMSLPTKISRCPHLLDFFKVRP
                                                                                                                                                                                         VEVVEKSESGWWFCQMKAKRGWIPASFLEPLDSPDETEDPEPNYAGEPYVAIKAYTAVEG
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                                                                                            DDLKLPTDNQTKKPETYLMPKDGKSTATDITGPIILQTYRAIANYEKTSGSEMALSTGDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels · 58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 275; DB 2;
; Pred. No. 8e-13;
46; Mismatches 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QPAVPPRPSADLILNRCSESTKRKLASAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VTGYFPSMYLQKSGQDVSQAQRQI--
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26.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         344 SPLEEERQTQRSKPQPAVPP
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Best Local Similarity 26.99
Matches 70; Conservative
```

RESULT

m

12;

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A; Description: probably functions as a scaffolding molecule with a specialized role 1 C; Keywords: coiled coil; homodimer
               A;Residues: 52-92;115-125;131-145;146,176-186;192-213;228-234;241-263;297-308;317-322
C;Superfamily: SH3 homology
C;Keywords: cytosol
F;177-224/Domain: SH3 homology <SH3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-699 <KTRS
A; Cross-references: EMBL.AF146277; NID:94960046; PID:94960047; PIDN:AAD34595.1
R; Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, March 1999
A; Reference number: 216471
A; Accession: T08754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C.Species: Homo sapiens (man)
C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Nov-2000
C.Accession: T13151; T08754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EDLSSTPLLKDLLELTRREFQREDIALN-YRDAEGDLVRLLSDEDVALMVRQARGLPSQ 316
                                                                                                                                                                                                                                                                                                                                                                                71 --IIPHLPAPKWFDG--QRAAENRQGTLTEYCSTLMSLPTKISRCPHLLDFFKVRP-DDL 125
                                                                                                                                                                                                                                                                                                                                                                                                                KLPTDNQTKKPETYLMPKDGKSTATDITGPIILQTYRAIANYEKTSGSEMALS--TGDVV 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EPNYAGEPY-------WAIKAYTAVEGDEVSLLEGEAVEVI------H 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45 TEIYEFHKTLKEMFPIEAGAINPENRIIPHLPAPKWFDGQRAAENRQGTLTEYCSTLMSL 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          168 TDDGETHEAQDDSETVLAGPTSP----IPSL------GNVSETASGSVTQ 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Kirsch, K.H.; Georgescu, M.M.; Ishimaru, S.; Hanafusa, H.
Proc. Natl. Acad. Sci. U.S.A. 96, 6211-6216, 1999
A;Title: CMS: An adapter molecule involved in cytoskeletal rearrangements.
A;Reference number: 217608; MUID:99272673
                                                                                                                                                                                                                                                                                                            15 EKRFVPSQHYVYMFLVKWQDLSEKVVYRRFTEIYEFHKTLKEMFPIEAGAINPENR---- 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 113;
                                                                                                                                                                           Length 339;
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A;Residuces: 548-639 <WAN>
A;Cross-references: EMBL.AL050105
A;Experimental source: adult uterus; clone DKFZp586H0519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.1%; Score 164.5; DB 2;
22.9%; Pred. No. 0.00011;
ative 50; Mismatches 127;
                                                                                                                                                                        8.3%; Score 169.5; DB 2; 24.4%; Pred. No. 2e-05;
                                                                                                                                                                                                                             48; Mismatches 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     184 EVVEKSESGWWFCQMKAKRGWIPASFLEPLDSPDETEDP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Accession: T13151
A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                Best Local Similarity 24.48
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             258 KLLDGWKDDVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             317 KRLFPWKLHIT
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                                                                                                                                                                           Query Match
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C.Species: Xenopus laevis (African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: T09194
R:Yamabhai, M.; Hoffman, N.G.; Hardison, N.L.; McPherson, P.S.; Castagnoli, L.; Cesareni
J. Biol. Chem. 273, 31401-31407, 1998
A;Title: Intersectin, a novel adaptor protein with two eps15 homology and five src homol
A;Reference number: 216605; MUID:99030416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Describes: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 19-May-1994 #sequence_revision 17-Nov-1995 #text_change 07-May-1999
C; Accession: S39768; S39769; S39769; S39769; S39769; S97561, 1993
Biochem. J. 296, 557-561, 1993
A; Title: p40(phox), a third cytosolic component of the activation complex of the NADPH cA; Reference number: S39768 MUID:94107216
A; Reference number: S39768
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-339 < WHE>
A; Residues: 1-339 < WHE>
A; Residues: 1-339 < WHE>
A; Rocession: S39769
A; Rocession: S39769
A; Rolecule type: protein
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                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRM
A;Residues: 1-1270 «YAM>
A;Cross-references: EMBL:AF032118; NID:g2642624; PIDN:AAC73068.1; PID:g2642625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  961 TSIDSTSSESPASLKRVSSPAFKPAIQGEEYISMYTYESNEQGDLTFQQGDLIVVIKKDG 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1021 DWWTGTVGEKTGVFPSNYVRPKDSEAAGSGGKTGSLGKKPEIAQVIASYAATAPEQLTL- 1079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       294 APPRRSSIRNAH-----SIHQRSRKRLSQDAYRRNSVRFLQQRRRQARPGPQSPGSPL 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84 ORAAENROGTLTEYCSTLMSLPT-KISRCP------HLLDFFKVRPDDLKLP 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             129 TDNQTKKPE-----TYLMPKDGKS-----TATDITG----PIILQ-----T 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         733 KVVYYR--ALYPFDARSHDEITIEPGDIIMVDE--SQTGEPGWLGGELKGKTGWFPANYA 788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :| |: : |: : | | : | ERMPESEFPSTIKPAAETIAKPTVHVAPSPVAPAAFTNTSTNSNNWADFSSTWP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 161 YRAIANYEKTSGSEMALSTGDVVEVVEKSESGWWFCQMKAKRGWIPASFLEPLDSP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DGWKDDV---TGYFPSMYLQ-----KSGQ-----DVSQ-----AQRQIKRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 8.8%; Score 179.5; DB 2; Length 1270; Best Local Similarity 21.1%; Pred. No. 2.2e-05; Matches 93; Conservative 66; Mismatches 135; Indels 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38 KVVYRRFTEIYEFHKTLKEMFPIEAGAINPENRIIPHLPAPKWFDG----
                                                                                                                                                                                                                                                                                                                                                                             A.Experimental source: cell type oocyte
C.Function:
A.Description: involved in endocytosis
C.Keywords: endocytosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----NKSTPTEPPKPTS 1137
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protein, CIN85, that interac
                                                      dynamin associated protein isoform Dap160-1 - fruit fly (Drosophila melanogaster) C; Species: Drosophila melanogaster C; Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000 C; Accession: T13053 R; Roos, J.; Kelly, R.B. J. Biol. Chem. 273, 19108-19119, 1998 A; Title: Dap160, a neural-specific Eps15 homology and multiple SH3 domain-containing A; Reference number: Z17594; MuID:98334647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15;
                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: EMBL: AF053957; NID: 92984714; PID: 92984715; PIDN: AAC39138.1
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C;Species: Homo sapiens (man)
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 23-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----TYRAIANYEKTSGSEMALSTGDV--VEVVEKSE 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    651 YAVASNDISALAAPAVDLGGPAPEGFVKYQAVYEFNARNAEEITFVPGDIILVPLEQNAE 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | | :: | : | :: | PGWLAGEINGHTGWFPESYVEKLEVGEVAPVAAVEAPVDAQVADTYNDNINTSSIPAASA 770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---ERQTQRSKPQPAVPPRPSADLILNRCSE 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      104 LPTKISRCPHLLDFFKVRPD----DLKLPTDNQTKKPETYLMPKDGKSTATDITGPIILQ- 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --YVAIKAYTAVEGDEVSLLEGEAVEVIHKLLDGWKDDV---TGYFPSMYLQ 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KSGQDVSQAQRQIKRGAPPRRS----SIRNAHSIHQRSRKRLSQDAYRRNSVRFLQQRRR 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --EPSEQPISSPGVGAEEAHEDLDTEVSQINTQSKTQSSEPAESY-SRP----MSRTSS 930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGWWFCQMKAKRGWIPASFLEPLDSPD--------ETEDPEPNYAGEP---
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R;Take, H.; Watanabe, S.; Takeda, K.; Yu, Z.X.; Iwata, N.; Kajigaya, Biochem. Biophys. Res. Commun. 268, 321-328, 2000
A;Title: Cloning and characterization of a novel adaptor protein, CID A;Reference number: JC7191; MUID:20145431; PMID:10679202
A;Accession: JC7191
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A;Molecule type: mRNA
A;Residues: 1-665 <TAK>
A;Cross-references: GB:AF230904; NID:g7188748; PID:g7188749
C;Genetics:
A;Gene: CIN85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 161; DB 2; L
Pred. No. 0.00045;
); Mismatches 125;
                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1094 <ROO>
                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: Dap160
A;Cross-references: FlyBase:FBgn0023388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.9%; Scor.
21.3%; Pred
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Matches 77; Conserv
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C; Specias: Drosophila melanogaster
C; Specias: Drosophila melanogaster
C; Specias: Drosophila melanogaster
C; Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
C; Accession: T13055
R; Roos, J.; Kelly, R.B.
J. Biol. Chem. 273, 19108-19119, 1998
A; Title: Dap160, a neural-specific Eps15 homology and multiple SH3 domain-containing pro
A; Reterence number: 217594; MUID: 98334647
A; Accession: T13055
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Accession: T13055
A; Status: Preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-1011 <ROO>
A; Cross-references: EMBL: AF054612; NID: 92996029; PID: 92996030; PIDN: AAC39139.1
C; Genetics:
A; Gene: Dap160
A; Cross-references: FlyBase: FBgn0023388
                             212 PL-----DSPDETEDPEPNYAGEP----YVAIKAYTAV---EGDEVSLLEGEAVEVIHKL 259
                                                                                                                                                                                                                                                                                     260 LDGWKDDVTGYFPSMYLQKSGQDVSQAQRQIKRGAPPRRSS--IRNAHSIHQRSRKRLSQ 317
                                                                                                                                                                                                                                                                                                                                                                                                                              -----KRPEKPVPPPPPIAKINGEVSSISSKFETEPVSKLKLDSEQLPLRP 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------TYRAIANYEKTSGSEMALSTGDV--VEVVEKSE 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YAVASNDISALAAPAVDLGGPAPEGFVKYQAVYEFNARNAEEITFVPGDIILVPLEQNAE 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----- ETEDPEPNYAGEP---- 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---PK--DGKSTATDITG 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104 LPTKISRCPHLLDFFKVRPD---DLKLPTDNQTKKPETYLMPKDGKSTATDITGPIILQ- 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            594 LSALITKCEDLYKEYDVQRTSVLELKYNRKNETSVSSAW----DTGSSSAWEETGTTVTDP 650
                                                                                              PIILQTY-RAIANYEKTSGSEMALSTGDVVEVVEK--SESGWWFCQMKAKRGWIPASFLE
                                                                                                                                                                                                                                                                                                                     ---QKPSKPAA-PQVPPKKPTPPTKASNLLRSSGTVYP----
                                                                                                                                                                                                                                                                                                                                                                                      ---GSPLEEERQTQRSKPQPAVPPRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PGWLAGEINGHTGWFPESYVEKLEVGEVAPVAAVEAPVDAQVADTYNDNINTSSIPAASA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----YVAIKAYTAVEGDEVSLLEGEAVEVIHKLLDGWKDDV---TGYFPSMYLO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        831 KA--DVGTASTAAAEPVESLDQGMRAKRSEIAQVIAPYEATSTEQLSLTRGQLIMIRKKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

8.1%; Score 164; DB 2; Length 1011;
Best Local Similarity 22.4%; Pred. No. 0.00024;
Matches 79; Conservative 42; Mismatches 121; Indels 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  889 DSGWWEGELQAKGRRRQIGWFPATYVKVLQGGRNSGRNTPVS-GSRIEMTEQ 939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----LSQDAYRR----NSVRFLQQRRRQARPGPQSPGSPLEEERQ 351
                                                                                                                                                                                                                                      327 QINELDKDFPKPKKPPPPAKAPAPKPELIAAEKKYFSLKPEEKDEKSTLE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KSGQDVSQAQ-----RQIKRGAPPRRSSIR-----NAHSIHQRS-
  PTKISRCPHLLDFFKVRPDDLKLPT -- - DNQTKKPETYLM --
                                                                                                                                                                                                                                                                                                                                                                                 318 DAYRRNSVRFLQQRRRQARPGPQSP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGWWFCQMKAKRGWIPASFLEPLDSPD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            457 KSVDFDSLTVRTSKET 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SA---DLILNRCSEST 378
                                               208
105
                                                                                              155
                                                                                                                                        267
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hypothetical protein Y116A8C.36 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T31504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        200 AKRGWIPASFLEPLDSPDETEDP-----EPNYAGEPYVAIKA-----YTAVEGDEVSLLE 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         140 LMPKDGKSTATDITGPIILQTYRAIANYEKTSGSEMALSTGDVVEVVEKSESGWWFCQMK 199
                                                                                                                                                                                                                                                                                                                                                       158 LQTYRAIANYEKTSGSEMALSTGDVVEVVEKS-ESGWWFCQMKAKR-----GWIPASF 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                               210 LEPLDSPDETEDPEPNYAGEPYVAIKAYTAVEGDEVSLLEGEAVEVIHKLLDGW----KD 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    266 DVTGYFPSMYLQKSGQD-----VSQAQRQIKRGAPPRRSSIRNAH--SIHQRSRKRLSQ 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112 GDYGFAPANYIESVPSEPSTPVAASNPAAAAIAGVMANRSSFQPPAPISVPQPQRQSYAS 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DAYRRNSVRFLQQRRRQARPGPQSP--GSPLEEERQTQRSKPQPA------VPPR 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        172 EDY-ENEVR-----SPPLPSRPRGDSQIAPEQKSYRPVPPAQSAAHDTDDYGISPR 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       937 GREGIFPANYVE--ISVQQAGDPTPPTQAPTPAAPPTVLCEAKVVVDFVASAPNQLGIKV 994
                                                                                                                                                                                                                                                                                                                                                                                                    4 LGVYRAIYDYTPQGEGELTISEGDILYVLEKSQEDDWWKAKKKANAADDDEPVGLIPNNY 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-1097 <MIL>
A;Cross-references: EMEL:ALIJ7204; PIDN:CAB55138.1; CESP:Y116A8C.36
A;Experimental source: clone Y116A8C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1097;
                                                                                                                                                                                                                                               Length 1119;
                         A,Cross-references: EMBL:AL389891; GSPDB:GN00116; NCSP:B7F18.140
A,Experimental source: BAC clone B7F18; strain OR74A
C;Genetics:
A;Gene: NCSP:B7F18.140
A;Map position: 6
A;Introns: 66/3; 123/2; 495/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: CESP:Y116A8C.36
A;Introns: 50/3; 245/3; 411/3; 486/3; 697/1; 820/3; 926/2
                                                                                                                                                                                                                                                                                               95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                            7.1%; Score 145; DB 2; 25.6%; Pred. No. 0.0076; ative 31; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.0%; Score 142.5; DB 26.3%; Pred. No. 0.011; tive 33; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;McMurray, A.
submitted to the EMBL Data Library, October 1999
A;Reference number: 221041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 26.3%
Matches 44; Conservative
                                                                                                                                                                                                                                                                                                    Conservative
     1-1119 <SCH>
                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 62; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64
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Cispecies: Neurospora crassa
Cispecies: Neurospora crassa
Cispecies: Neurospora crassa
Cispecies: 11-12000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000
Cispecies: 17-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000
Cispecies: November 150995
Rischulte, U.; Algn, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, Submitted to the Protein Sequence Database, July 2000
A; Reference number: 225286
A; Accession: T50995
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                742526
hypothetical protein - fission yeast (Schizosaccharomyces pombe) (fragment)
C:Species: Schizosaccharomyces pombe
C:Species: Schizosaccharomyces pombe
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000
C:Accession: T42526
R:Yoshioka, S: Kato, K.; Nakai, K.; Okayama, H.; Nojima, H.
DNA Res. 4, 363-369, 1997
A:Title: Identification of open reading frames in Schizosaccharomyces pombe cDNAs.
A:Reference number: Z17323; MUID:98162722
A:Accession: T42526
A:Status: preliminary; translated from GB/EMBL/DDBJ
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A;Experimental source: strain PR745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    132 VPPLPPHDETQEPQV-----GGDVKATEHTQPTKTPAI-VIYDYSPEEENEIELVENEQI 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 DLKLPTDNQTKKPETYLMPKDGKSTATDITGPIILQTYRAIANYEKTSGSEMALSTGDVV 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              166 NYEKTSGSEMALSTGDVVEVVEKSESGWWFCQMKAKRGWIPASFLEPLDSPDETEDPEPN 225
                                                                                                                                                                                                                        -----YVAIKAYTAVEGDEVSLLEGEAVE 254
                                                                                                                                                                                                                                                                              68 KAPEKPLHEVPSGNSLLSSETILRTNKRGERRRRRCQVAF-SYLPQNDDELELKVGDIIE 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 AINPENRIIPHLPAPKWFDGQRAAENRQGTLTEYCSTLMSLPTKISRCPHLLDFFKVRPD 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 111 FLKPP--AVPVVPEP-----PV 131
                                                                                                                                            5 FIRHIALLGFEKRFVPSQHYVYMFLVKWQDLSEKVVYRRFTEIYEF-HKTLKEMFPIEAG 63
                                                                                                                                                                                                                                                                                                                                                          255 VIHKLLDGWKDDV----TGYFPSMYLQK-SGQD----VSQAQRQIKRGAPPRRSSIR 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184 EVVEKSESGWWFCQ-MKAKRGWIPASFLEPLDSPDETED--PEPNYAGEPYVAIKA---Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 290;
     Length 665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 7.2%; Score 147.5; DB 2; Length Best Local Similarity 20.7%; Pred. No. 0.00074; Matches 59; Conservative 56; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            245 QAQEDNELSFFEDEIIANVDCVDPNWWEGECHGHRGLFPSNYVEE 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          238 TAVEGDEVSLLEGEAVEVIHKLLDGWKDDV----TGYFPSMYLQK 278
7.4%; Score 150.5; DB 2; 24.3%; Pred. No. 0.0014; tive 34; Mismatches 51;
                                                        Conservative
                              Local Similarity
nes 43; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-290 <YOS>
                                                                                                                                                                                                                        226 YAGEP---
        Query Match
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hypothetical protein DKFZp586P1422.1 - human
C;Species: Homo sapiens (man)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AVKRESDGAPGDLTSLENERQIYKSVLEGGDIPLQGLSGLKRPSSSASTKDSESPRHFIP 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----PETY--LMPKDGKSTATDITGPIILQTYRAIA--NYEKTSGSEMALSTGDVVE 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     618 HGRVGIFPRTYIELLPPAEKAQPKKLTPVQVLEYGEAIAKFNFNGDTQVEMSFRKGERIT 677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :: : : | |: :: :: :: | | :::: |: |: | LRQVDENWYEGRIPGTSRQIFPITYUDVIKRPLVKNPVDYMDLPFSSSPSRSATASPQ 737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----SPDETEDPEPNYAGEPYVAIKAYTAVEGDEVSLLEGEAVEVIHKLLDGW-- 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QPQAQQRRVTPDRSQTSQDLFS---YQALYSYIPQNDDELELRDGDIVDVMEKCDDGWFV 794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32 WODLSEKVVYRRF----TEIYEFHKTLKEMFPIE--AGAINPENRIIPHLP----APKWF 81
                                                                                                                                                                                                                                                                                                                  C;Accession: T17257
R;Koehrer, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, submitted to the Protein Sequence Database, September 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VVEKSESGWWFCQM--KAKRGWIPASFLE------PLD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Experimental source: adult uterus; clone DKFZp586P1422 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.7%; Score 135.5; DB 2;
19.3%; Pred. No. 0.026;
live 57; Mismatches 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----DFFKVRPDD-----LKLPTDNQTKK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82 DGQRAAENRQGTLTE-----YCSTL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch completed: January 11, 2002, 09:08:16 time: 142 sec
    MGDTFIRHIALLGFEKRFVPSQHYVHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: EMBL: AL117472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----KDDVTGYFPSMYLQ 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTSRRIKOFGTFPGNYVK 812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 19.38
Matches 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Reference number: Z18722
A;Accession: T17257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-816 <KOE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Note: DKFZp586P1422.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          498
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A58214
neutrophil cytosol factor 1 frameshift mutant - human
N;Alternate names: 47K autosomal chronic granulomatous disease protein; NCF-47K protein;
C;Species: Homo sapiens (man)
C;Species: Homo sapiens
R;Casimir, C.M.; Bu-Ghanim, H.N.; Rodaway, A.R.F.; Bentley, D.L.; Rowe, P.; Segal, A.W.
Proc. Natl. Acad. Sci. U.S.A. 88, 2753-2757, 1991
A;Title: Autosomal recessive chronic granulomatous disease caused by deletion at a dinucle A;Reference number: 159190; MUID:91187870
A;Accession: A58224
A;Molecule type: mRNA
A;Molecule type: Ranslation is not annotated in GenBank entry HUMPHOXE25, release 113.0
A;Accession: 179641
A;Status: translated from GB/EMBL/DDBJ
A;Accession: 75432 Annotation
A;Accession
A;Accessio
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0
                                                                    Species: Caenorhabditis elegans
Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 167 NYVEEVEASTNGNOGSIENRNPAAAAVPAPIMMQAPPPKLQASRSSFEVVVALYSFDASS 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SFLEPLD-----EPYVAIKAYTAVE 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           155 PIILQTYRAIA--NYEKTSGSEMALSTGDVVEVVEKSESGWWFCQMKAKR----GWIPA 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242 GDEVSLLEGEAVEVI----HKLLDGW----KDDVTGYFPSMYLQKSGQDVSQAQRQIKRG 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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A;Cross-references: GB:M60942; NID:g189950; PIDN:AAA60087.1; PID:g553612
            Apportetical protein ZK470.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 12-Cot-1999 #sequence_revision 15-Oct-1999 #text_change 15-C
C;Accession: T27877
R;Minx, P.
submitted to the EMBL Data Library, October 1995
A;Description: The sequence of C. elegans cosmid ZK470.
A;Reference number: 220433
A;Accession: T27877
A;Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 6.8%; Score 139; DB 2; Length 44 Best Local Similarity 24.7%; Pred. No. 0.0059; Matches 45; Conservative 29; Mismatches 62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 50;
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Pred. No. 0.00048;
2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.7%;
ilarity 92.6%;
Conservative
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A;Cross-references: GDB:120222
A;Map position: 7q11.23-7q11.23
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Best Local Simi
Matches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11
AP 287
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6

16;

Gaps

Indels 135; Length 816;

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GenCore version 4.5
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OM protein - protein search, using sw mode

January 11, 2002, 09:05:54 Run on:

; Search time 25.33 Seconds
(without alignments)
1128.792 Million cell updates/sec

US-09-820-005-2 2035 Title: Perfect score:

1 MGDTFIRHIALLGFEKRFVP......ADLILNRCSESTKRKLASAV 386 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

522463 Total number of hits satisfying chosen parameters:

522463 seqs, 74073290 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

A_Geneseq_1101:* Database

| SIDSB/gcgdata/geneseq/geneseqp/AA1980.DAT:*
| SIDSB/gcgdata/geneseq/geneseqp/AA1981.DAT:*
| SIDSB/gcgdata/geneseq/geneseqp/AA1982.DAT:*
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| SIDSB/gcgdata/geneseq/geneseqp/AA1985.DAT:*
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/SIDS8/gcgdata/geneseg/genesegp/AA1994.DAT: /SIDS8/gcgdata/geneseg/genesegp/AA1995.DAT:

/SIDS8/gcgdata/geneseg/genesegp/AA1996.DAT

/SIDS8/gcgdata/geneseq/geneseqp/AA1997

1

					SUMMARIES	
		÷				
Result		Query	Query			
NO.	Score	Match	Length	DB	ID	Description
-	2006	98.6		16	AAR83825	p47(phox) protein.
7	691	34.0		22	AAG64031	Human PX domain.
3	688	33.8	128	22	AAG64033	Human PX domain-re
4	593	29.1		21	AAB53681	Human colon cancer
5	305	15.0		22	AAG64032	Human SH3 domain.
9	295	14.5		22	AAG64034	Human SH3 domain-r
7	261	12.8		22	AAU14174	Human novel protei
ω	188	9.5		17		Human clone 65 pro
0	187	9.5		21		Human ORFX ORF747
10	183	9.0	-	21		Rat phosphodiester
11	177.5	8.7	_	21		Mouse Ese2 protein

Mouse Ese2L protei	Human SH3P18 prote	Mouse Esel protein	Mouse EselL protei				Human SH3D1A prote		Human NNG2 (long f	Human NNG2 (short		associated i	associated	iated	Human CD2 associat	Candida albicans C	associated	-associated	CD2 associated int	an CD2 assoc	CD2 associated int	CD2-associated int	•	an CD2	CD2 associated int		Amino acid sequenc	Amino acid sequenc	Human polypeptide	431 (	Protein of the inv	cid seque	Murine tyrosine ph
AAY57450	AAW05396	AAY57444	AAY57449	AAY32156	AAY32155	9	AAY32158	AAY32154	AAB19691	AAB19690	AAB19685	AAW26497	AAW25117	AAW80421	AAB66392	AAW48898	AAW26496	AAW25116	AAW80420	AAB66391	σ	AAW25115	AAW80419	6	AAW37724	AAY28292	AAY28291		$\vdash$	AAY99428	7	AAB19313	AAW71595
21	17	21	21	20	20	17	20	20	21	21	21	18	18	20	22	19	18	18	20	22	18	18	20	22	19	20	20	21	22	21	22	21	19
1658	248	21	1715	1215	22	462	641	1144	709	665	665	324	324	324	324	635	464	464	464	464	553	553	553	553	629	397	416	416	1035	370	37	1200	415
8.7	8.7						7.7			7.4									•													9.9	
177.5	176.5	172	168.5	167	166	157	157	157	156.5	150.5	150			47.		•	4	144	144	144	141	141	141	141	141	37	37	$\sim$	34	33	3	133.5	$^{\circ}$
12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

p47(phox); p67(phox); NADPH oxidase complex; proline-rich region; PTPase; St3 domain; inhibition; dynamin; cytochrome b245; reperfusion injury; septic shock; arthritis; asthms; vinculin; inflammatory bowel disease; adult respiratory distress syndrome; ischaemic heart disease. /label= OTHER /note= "designated O in specification" 360..3 /note= "proline-rich region used to design inhib" /note= "designated O in specification" Misc-difference 197 Location/Qualifiers 22 AAR83825 standard; Protein; 390 AA. (first entry) p47(phox) protein. Misc-difference Homo sapiens 15-FEB-1996 AAR83825 Region AAR83825 RESULT 

94GB-0024674 07-DEC-1994; GB2285047-A 28-JUN-1995

94GB-0000248.

07-JAN-1994;

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Homo sapiens
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                                                                           14-JUN-2001
                                                                                                                                                              Kohda D,
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                               The protein p47(phox) (AAR83825) interacts with protein p67(phox) in the NADPH oxidase complex via a C-terminal proline-rich region of p47(phox) binding to at least one C-terminal SH3 domain of p67(phox). The peptides AAR83814-24 were derived from the proline-rich region of p47(phox) and show inhibitory activity towards the binding of p47(phox) to p67(phox) as compared to the proline-rich region of a range of other proteins (AAR83826-30). The inhibitory peptides can be used for the treatment of chronic or acute inflammatory diseases e.g. septic shock, arthritis, asthma, adult respiratory distress syndrome, ischaemic heart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; antiinflammatory; protein coordinate data; chemical shift data; nuclear magnetic resonance; NMR; structural coordinate data;
                                                                                                                                                                                                                                                                                                                                                                                                    180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EAGAINPENRIIPHLPAPKWFDGQRAAENRQGTLTEYCSTLMSLPTKISRCPHLLDFFKV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                 RPDDLKLPTDNQTKKPETYLMPKDGKSTATDITGPIILQTYRAIANYEKTSGSEMALSTG 180
                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                         1 MGDTFIRHIALLGFEKRFVPSQHYVYMFLVKWQDLSEKVVYRRFTEIYEFHKTLKEMFPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DVVEVVEKSESGWWFCQMKAKRGWIPASFLEPLDSPDETEDPEPNYAGEPYVAIKAYTAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EGDEVSLLEGEAVEVIHKLLDGW----KDDVTGYFPSMYLQKSGQDVSQAQRQIKRGAPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RRSSIRNAHSIHQRSRKRLSQDAYRRNSVRFLQQRRRQARPGPQSPGSPLEEERQTQRSK
                                                                                                                                                                                                                                                                                                                           4;
                                                                                              polypeptide(s) with antiinflammatory action - inhibit NADPH
                                                                                                                                                                                                                                                                                                   98.6%; Score 2006; DB 16; Length 390; 98.2%; Pred. No. 8.5e-187; 1ve 1; Mismatches 2; Indels 4
                                                     Waterfield MD;
                                                                                                                                                                                                                                                disease, reperfusion injury or inflammatory bowel disease.
                                                     Shimizu Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PQPAVPPRPSADLILNRCSESTKRKLASAV 386
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                                                                                                                             Example 1; Fig 1; 17pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAG64031 standard; protein; 128
                     (LUDW-) LUDWIG INST CANCER RES (YAMA ) YAMANOUCHI UK LTD.
                                                     Kellie S,
93GB-0026083
                                                                                                                                                                                                                                                                                                              Best Local Similarity 98.2
Matches 383; Conservative
                                                    Gout IT,
                                                                         WPI; 1995-217703/29
                                                                                                                                                                                                                                                                      390 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human PX domain.
                                                                                                           system
21-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-SEP-2001
                                                     Finan PM,
                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                               New
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The present sequence is provided in a specification relating to the use of chemical shift data from nuclear magnetic resonance (NMR) and structural coordinate data of the PX domain of a protein to search for, evaluate, design and identify variant PX domain sequences for controlling the function of proteins containing the PX domain. It also relates to compounds promoting the binding of substances to the PX domain, and compounds inhibiting the binding of substances to the PX domain. The invention can be used in the identification of substances that can be used in the regulation of reduced nicotinamide adenine dinucleotide phosphate (NADPH) oxidase activity, which is involved in superoxide production in inflammatory response in disease or trauma.
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PX domain; reduced nicotinamide adenine dinucleotide phosphate; NADPH;
NADPH oxidase; superoxide production; inflammatory disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Regulation of function of a protein containing a PX domain for controlling an inflammatory response to disease or trauma, comprises using nuclear magnetic resonance (NMR) chemical shift and structural coordinate data
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100.0%; Pred
0; M
                                                                                                                                                                                                                                                                                                                                                                                                                                               (BIOM-) BIOMOLECULAR ENG RES INST.
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Matches 128; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hiroaki H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-381679/40.
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rpddlklp 128
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Homo sapiens.
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                                                                                                                                                                                                                                                                 The present sequence is provided in a specification relating to the use of chemical shift data from nuclear magnetic resonance (NMR) and structural coordinate data of the PX domain of a protein to search for, evaluate, design and identify variant PX domain sequences for controlling the function of proteins containing the PX domain. It also relates to compounds promoting the binding of substances to the PX domain, and compounds inhibiting the binding of substances to the PX domain. The invention can be used in the identification of substances that can be used in the regulation of reduced nicotinamica adenine dinucleotide phosphate (RADPH) oxidase activity, which is involved in superoxide production in inflammatory response in disease or trauma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 identification: cytostatic; cardioactive; neuroprotective; vulnerary; immunomodulatory; muscular; gynaecological; gastrointestinal; nephrotropic; antinfective; antibacterial; gene therapy; wound; neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; renal disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 EAGAINPENRIIPHLPAPKWFDGQRAAENRQGTLTEYCSTLMSLPTKISRCPHLLDFFKV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                    Regulation of function of a protein containing a PX domain for controlling an inflammatory response to disease or trauma, comprises using nuclear magnetic resonance (NMR) chemical shift and structural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MGDTFIRHIALLGFEKRFVPSQHYVYMFLVKWQDLSEKVVYRRFTEIYEFHKTLKEMFPI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; colon cancer; colon cancer antigen; diagnosis; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 688; DB 22; Length 128;
Pred. No. 4e-59;
1; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human colon cancer antigen protein sequence SEQ ID NO:1221.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               infectious disease; cardiovascular disorder.
                                                                                                                                                                                                                                               Example 3; Page 186; 195pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB53681 standard; Protein; 141 AA.
                                                                                                                 (BIOM-) BIOMOLECULAR ENG RES INST
                                                                                                                                          Sumimoto H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --
                                                                                                                                                                                                                                                                                                                                                                                                                                                 33.8%;
99.2%;
                                                                    01-DEC-2000; 2000WO-JP08501
                                                                                           99JP-0346193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127; Conservative
                                                                                                                                          Kohda D, Hiroaki H,
                                                                                                                                                               WPI; 2001-381679/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                128 AA
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                                                                                                                                                                                                                          coordinate data
                       WO200142453-A1.
 Homo sapiens.
                                                                                           06-DEC-1999;
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                                              14-JUN-2001
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Best Local Si
Matches 127;
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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AAC97991 to AAC98763 encode the human colon cancer associated proteins, called human colon cancer antigens, given in AAB3234 to AAB54006. The human colon cancer antigens can have cytostatic, cardioactive, muscular; neuroprotective, immunomodulatory, gynaecological, gastrointestinal, vulnerary, nephrotropic, antiinfective and antibacterial activities, and can be used in gene therapy. The colon cancer antigen polynoucleotides, proteins and antibodies to the proteins are useful for the prevention, treatment and diagnosis of colon disorders, such as colon cancer. The polynucleotides may be used in diagnostics and research, such as for chromosome identification, and as hybridisation probes. The proteins may also be used to prevent disorders, reproductive disorders, immune system disorders, muscular disorders, reproductive disorders, immune system disorders, wounds, renal disorders, infectious diseases, and cardiovascular disorders. AAC98764 to AAC98772 and AAB54007 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; antiinflammatory; protein coordinate data; chemical shift data; nuclear magnetic resonance; NMR; structural coordinate data; PX domain; reduced nicotinamide adenine dinucleotide phosphate; NADPH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Colon cancer associated gene sequences, referred to as colon cancer antigens, useful for the treatment, prevention, and diagnosis of colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAINPENRIIPHLPAPKWFDGQRAAENRQGTLTEYCSTLMSLPTKISRCPHLLDFFKVRP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 DTFIRHIALLGFEKRFVPSQHYVYMFLVKWQDLSEKVVYRRFTEIYEFHKTLKEMFPIEA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 593; DB 21; Length 141;
Pred. No. 8.3e-50;
7; Mismatches 16; Indels 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 11; Page 1810-1811; 2104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disorders such as colon cancer
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                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                     38-MAR-2000; 2000WO-US05883.
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                                                                                                                                                                                                                                                                                                                                             Rosen CA, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-587534/55.
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Matches 118; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seguence 141 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAC98438
WO200055351-A1.
                                                                                                                                                                                                        12-MAR-1999;
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                                                                      21-SEP-2000
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The present sequence is provided in a specification relating to the use of chemical shift data from nuclear magnetic resonance (NMR) and structural coordinate data of the PX domain of a protein to search for, evaluate, design and identify variant PX domain sequences for controlling the function of proteins containing the PX domain. It also relates to compounds promoting the binding of substances to the PX domain, and compounds inhibiting the binding of substances to the PX domain. The invention can be used in the identification of substances that can be used in the regulation of reduced nicotinamide adenihe dinucleotide phosphate (NADPH) oxidase activity, which is involved in superoxide production in inflammatory response in disease or trauma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           223 EPNYAGEPYYAIKAYTAVEGDEVSLLEGEAVEVIHKLLDG-W---KDDVTGYFPSMYLQK 278
                                                                                                                                                                                                                                                                                                                                                                                            controlling an inflammatory response to disease or trauma, comprises using nuclear magnetic resonance (NMR) chemical shift and structural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Regulation of function of a protein containing a PX domain for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 4; Page 188; 195pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU14174 standard; Protein; 968 AA.
                                                                                                                                                                   (BIOM-) BIOMOLECULAR ENG RES INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.5%;
                                    01-DEC-2000; 2000WO-JP08501.
                                                                                                    99JP-0346193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human novel protein #45.
                                                                                                                                                                                                                                  Hiroaki H,
                                                                                                                                                                                                                                                                                              WPI; 2001-381679/40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           coordinate data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200155437-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGQD 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |||||
sgqd 64
                                                                                                    06-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU14174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                  Kohda D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU14174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
      δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THO SECTION TO SECTION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is provided in a specification relating to the use of chemical shift data from nuclear magnetic resonance (NMR) and structural coordinate data of the PX domain of a protein to search for, evaluate, design and identify variant PX domain sequences for controlling the function of proteins containing the PX domain. It also domain, and compounds promoting the binding of substances to the PX domain. The invention can be used in the identification of substances that can be used in the regulation of reduced nicotinamide adenine dinucleotide phosphate (NADPH) oxidase activity, which is involved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; antiinflammatory; protein coordinate data; chemical shift data; nuclear magnetic resonance; NMR; structural coordinate data; PX domain; reduced nicotinamide adenine dinucleotide phosphate; NADPH; SH3 domain; NADPH oxidase; superoxide production; inflammatory disease.
NADPH oxidase; superoxide production; inflammatory disease; SH3 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Regulation of function of a protein containing a PX domain for controlling an inflammatory response to disease or trauma, comprises using nuclear magnetic resonance (NMR) chemical shift and structural coordinate data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            superoxide production in inflammatory response in disease or trauma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 305; DB 22; Length 64;
Pred. No. 2.8e-22;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 2; Page 183; 195pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAG64034 standard; Protein; 64 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sumimoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity 93.8%;
Matches 60; Conservative (
                                                                                                                                                                                                                                                          01-DEC-2000; 2000WO-JP08501
                                                                                                                                                                                                                                                                                                                      99JP-0346193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hiroaki H,
                                                                                                                                                                                                                                                                                                                                                                                     (BIOM-) BIOMOLECULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-381679/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 AA;
                                                                                                                        WO200142453-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200142453-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     279 SGQD 282
                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                      06-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 sgqd 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                                                                                          14-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kohda D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAG64034;
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4; Gaps

Length 64; Indels

Score 295; DB 22; Pred. No. 2.7e-21; Oreman 0;

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Human; novel protein; Antianaemic; osteopathic; antiinflammatory; immunomodulatory; cytostatic; neuroprotective; vulnerary; notropic; anticonvulsant; antiarthritic; cerebroprotective; antiinngal; antiviral; antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic; thrombolytic; immunogen; antibody; gene therapy; neurological disorder; parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis; tissue regeneration; immune disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-JAN-2001; 2001WO-US02623.
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14-JUN-2001

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The invention relates to polynucleotides encoding novel human proteins or their active domains. The polypeptides, polynucleotides and antibodies raised against the polypeptides are used in a method of treatment of a mammal and prevention of disorders caused by the aberrant protein expression or activity. The polypeptides can be used as molecular weight markers, food supplements, and in antibody production. The polypeptides are used to identify compounds which bind to the polypeptides. Polynucleotides of the invention are used as probes and primers, for sequencing, for chromosome or gene mapping, in the production of recombinant proteins, and in generating anti-sense DNA or RNA and in gene therapy. Polypeptides of the invention can be used to target drugs to a tumour, in assays to determine biological activity, to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein levels, as tissue markers, and to isolate receptors or ligands. Oblypeptides of the invention may also be useful in treating platelet disorders, stem cell disorders, regenerating bone, cartilage, tendon, ligament and/or nerve tissue, wound healing, treating burns, promoting the proliferation, differentiation and survival of stem cells, as a contraceptive, treating osteoporosis and osteoarthritis, anamia, Alzhelmer's, Parkinson's and Huntington's diseases, amylotrophic lateral sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         raise antibodies/elicit an immune response, to determine quantitative
                                                                                                                                                                                                          Isolated polypeptides useful for treating anti-inflammatory diseases, nervous system disorders, and for regenerating bone and cartilage -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fungal infection or from autoimmunity, cancer, allergy, asthma, graftversus.host disease, eczema, haemophilia, thrombosis, anti-inflammatory diseases, nervous system disorders, and infection. The present sequence represents a protein of the invention.
                                                                                                                                                                                                                                                                                         Example 4; Page 551-552; 894pp; English.
                                                                               Liu C, Drmanac RT;
                                                                                                                                WPI; 2001-451939/48.
                        HYSEQ INC
                                                                                                                                                           N-PSDB; AAS22479
                                                                       Tang YT,
                           (HYSE-)
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968 AA; Sequence

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                                                                                                                                                                                              290
                                                                                                                                                   156 IILQTYRAIANYEKTSGSEMALSTGDVVEVVEKSESGWWFCOMKAKRGWIPASFLEPLDS 215
                                                                                                                                                                                                                           121 gfekgvtvevirknlegwwyirylgke---gwapasylkkakddlptrkknlagpveiig 177
                                                                                                                                                                                                                                                         -----EPYVAIKAYTAVEGDEV
                                                                                                                                                                                            246 SLLEGEAVEVIHKLLDGW-----KDDVTGYFPSMYLQKSGQDVSQAQRQI-----
                                                                                                                                                                                                                                                                                       178 nimeisnllnkkasgdketppaegegheapiakkeislpilcnasngsavgvpdrtvsrl
                                      86;
12.8%; Score 261; DB 22; Length 968; 24.3%; Pred. No. 3.5e-16; Live 46; Mismatches 86; Indels 86
                                                                                                                                                                                                                                                                                                                                          316 SQDAYRRNSVRFLQQRRRQARPGPQSPGSPLEEERQTQRSKPQPAVPP 363
 Query Match 12.8'
Best Local Similarity 24.3'
Matches 70; Conservative
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AAW05399 standard; Protein; 509 AA.

AAW05399

AAW05399
ID AAW0:
XX
AC AAW0:
XX

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homology among known SH3 proteins. It has been found that small peptide RUs in multivalent form have reduced specificity for a given functional domain compared to monomer RUs. Multivalent RU complexes are particularly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW05386-W05403 represent novel human and mouse Src-homology region 3 (SH3) domain containing proteins that can be used in the method of the invention. SH3 domain containing proteins play a role in signalling and structural elements of cells. The method of the invention is for identifying polypeptides containing functional domains of interest (especially SH3 domains). The method comprises contacting a multivalent recognition unit (RU) complex with a number of peptides and identifying polypeptides having a selective binding affinity for the RU complex. The method is based on functional similarities and does not rely on sequence similarities. Prior methods only gave limited success for identifying proteins which contain an SH3 domain due to the minimal sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              suited to screening for polypeptides containing functional domains that are similar to, but not identical in sequence to, the original target functional domain. The new method enables proteins having a common function to be identified. Identification of novel SH3 proteins will be useful for a better understanding of cell growth, malignancy, signal transduction processes, etc. New candidate drugs can be identified, and their specificities (e.g. pharmacological activities) can be assessed using the method of the invention.
                                                                             Src-homology region 3 domain; human; mouse; SH3 domain; cell growth; cellular signalling element; cellular structural element; mailgnancy; protein identification; functional domain; protein screening; cellular signal transduction process.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 AINPENRIIPHLPAPKWFDGQRAAENRQGTLTEYCSTLMSLPTKISRCPHLLDFFKVRPD 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------ptvslsatstsseplssngpasvtdygnvsfs 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 DLKLPTDNQTKKPETYLMPKDGKSTATDITGPI-----ILQTYR--AIANYEKTSGSEMA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nltvntswqkksaft-----rtvspgsvspihgggqvenlkagalcswtakkdnhln 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     177 LSTGDVVEVVEKSESGWWFCQMKAKRGWIPASFLEPLDSPD-ETEDPEPNYA----- 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying polypeptide(s) having specific functional domain (esp. SH3 domain) - comprises detecting selective binding to recognition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sparks AB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58; Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mcconnell SJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9.2%; Score 188; DB 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unit, regardless of sequence homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Каў ВК,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 54; Fig 59; 174pp; English.
                                                                                                                                                                                                                                                                                                              96WO-US04454.
                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYNC-) UNIV NORTH CAROLINA.
                                                                                                                                                                                                                                                                                                                                                    96US-0630915.
19-FEB-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fowlkes DM, Hoffman N,
                                          Human clone 65 protein.
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| 141 avspkkallp-
                                                                                                                                                                                                                            WO9631625-A1.
                                                                                                                                                                                                                                                                                                              04-APR-1996;
                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                       03-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                          07-APR-1995;
                                                                                                                                                                                                                                                                     10-0CT-1996
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Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coaqulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; solution; severe compliabetic antidiabetic; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinutia; burn; wound; bone damage; cartilage damage; antidiflammatory disease; coaqulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAC7446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; antionvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating
            fskhdiltvleggen-wwfgevhggrgwfpksyvkilpgsevkreepealyaavnkkpts 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel nucleic acids and peptides derived from open reading frame X,
                                                          ----GEPYVAIKAYTAVEGDEVSLLEGEAVEVIHKLLDGWK---DDVTGYFPSMYLQKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease
                                                                                                                                                                                                                                                                                        Human ORFX, ORF747 polypeptide sequence SEQ ID NO:1494.
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                                                                                                280 GQDVSQAQRQIKRGAPPRRSSIRNAHSIHQRS 311
                                                                                                                  |: : | | | : | | : | dqesfgsas--ksgasnkkpeiaqvtsayvas 384
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                                                                                                                                                                                                    AAB40983 standard; Protein; 438
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99US-0127636.
99US-0127728.
2000US-0540763.
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                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                thrombosis; contraceptive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-MAR-1999;
02-APR-1999;
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                                                                                                                                                                                                                                   AAB40983;
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AAB40983
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pathological conditions associated with an ORFX-associated disorder. The
                               nucleic acids can be used to express ORFY proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal hæemoglobinuria, antlinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              112 PHLLDFFKVRP---DDLK--LPTDNQTKKPETYLMPKDGKSTATDITGPIILQTYRAIAN 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---grfegrpvpdgdakqrspkmrqrppprrdmtiprglnlpkppippqveeeyytiae 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LQKSGQD-----VSQAQRQIKRGAPPRRSS-IRNAHSIHQRSRKRLSQDAYRRNSV 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52 KTLKEMFPIEAGAINPENRIIPHLPAPKWFDGQRAAENRQGTLTEYCSTLMSLPTKISRC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 knsgeplppkpgpgspsh-----pgaldldgvsrqqnavgrekellssgrd-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176 laplphevtqlrlgeaaalenntgseatgpsrplpdaphgvmdsglpwskdwkg--skdv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            167 YEKTSGSEMALSTGDVVEVVEKSESGWWFCQMKAKRGWIPASFLEPLDSPDETEDPEPNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -AGEPY----VAIKAYTAVEGDEVSLLEGEA---VEVIHKLLDG----WKDDVTGYFPSMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.2%; Score 187; DB 21; Length 438; 33.6%; Pred. No. 1.7e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             234 lrkassdmsasagyeeisdpdmeekpslpprkesiiksegellererer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----qrteqlrgptpkppgvilpmmpakhippardsrrpepkp 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47; Mismatches 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rat phosphodiesterase interacting protein, M14.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 23.6%
Matches 81; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      438 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200027861-A1.
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04 - NOV - 1999
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ID AAY5
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                                                                                                                                                                                               The present sequence is a phosphodiesterase (PDE) interacting protein, M14 from rat. The protein modulates the functions and properties of PDEs, specifically cAMP-PDEs, and also targets them to specific subcellular
                                                                                                                                                                                                                                  compartments. The present sequence can be used in the diagnosis and treatment of disease conditions associated with PDE activity. The diseases include asthma, oystic fibrosis, inflammatory airway disease, chronic bronchitis, eosinophilic granuloma, psoriasis, proliferative skin diseases, endotoxic shock, septic shock, ulcerative colitis, Orohn's disease, reperfusion injury, inflammatory arthritis, atopic dermatitis, urticaria, adult respiratory distress syndrome, diabetes insipidus, allergic rhinitis, allergic conjunctivitis, vernal conjunctivitis, arterial restenosis,
                                                                                                                                                                                                                                                                                                                                                 atherosclerosis, inflammatory diseases associated with irritation and pain, rheumatorid arthritis, ankylosing spondylitis, transplant rejection and graft versus host disease, disease conditions associated with hypersecretion of gastric acid, and disease conditions in which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            162 RAIANYEKTSGSEMALSTGDVVEVVEKSESGWWFCQMKAKRGWIPASFLEPLDSPD-ETE 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----GEPYVAIKAYTAVEGDEVSLLEGEAVEVIHKLLDGWKDDV 267
                                                                                                                      Polynucleotide encoding a phosphodiesterase (PDE) interacting polypeptide, useful for diagnosis and treatment of asthma, cystic fibrosis, Crohn's disease, and rheumatoid arthritis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse; murine; Esel; Ese2; endocytosis; vesicular trafficking; regulation; actin cytoskeleton; detection; cancer; infection; i.H-domain and SH3-domain regulator of endocytosis; anticancer; antiproliferative; antiviral.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1683;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---TGYFPSMYLQ-KSGQDVSQAQRQIKRGAPPRRSSIRNAHSIHQRS 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 9.0%; Score 183; DB 21;
Best Local Similarity 28.0%; Pred. No. 3.2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37; Mismatches
                                               (STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY57445 standard; Protein; 1197 AA.
                                                                                                                                                                        Disclosure; Fig 6; 77pp; English.
99WO-US26860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse Ese2 protein sequence.
                       98US-0108255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                   cytokines are mediators.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             221 DPEPNYA------
                                                                                               WPI; 2000-376479/32.
                                                                       Conti M, Pahlke G;
                                                                                                                                                                                                                                                                                                                                                                                                                           1683 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9955728-A2.
12-NOV-1999;
                       12-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47;
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Matches
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The present sequence represents mouse Ese2. The present invention
specifically describes mammalian Esel and 2 proteins (1) and their splice
variants (Ese = EH-domain and SH3-domain regulator of endocytosis). (1)
are involved in regulation of clathrin-mediated endocytosis (as a complex
with Esp15 protein), vesicular trafficking and actin cytoskeleton.
Comerally (1) for its (ant)agonists, mimetics, fragments and inactive
mutants); (1)-specific antibodies (Ab); sequences antisense to the (I)
polynucleotide; agents that downregulate expression of Ese genes or
antagonists of an Ese binding partner are used to treat diseases
associated with undesirable endocytosis and resulting changes in cellular
function. Particularly overexpression of Esel is used to block
clathrin-mediated endocytosis in vivo or in cell cultures, while
administration of (I) is used to promote endocytosis of selected cells.
(Ant)agonists of (I) or Ab are used to suppress abnormal proliferation of
cells that can be stimulated to proliferate by a growth factor receptor;
and similar compounds (also inactive Ese mutants) can be used to prevent
viral infection. Endocytosis may also be regulated, in vivo or in cell
cultures, by forming an Ese Esp15 complex, then binding dynamin to the
complex. Generally conditions that can be treated include cancer;
complex. Generally conditions that can be treated include cancer;
complex selected electron or migration; viral infection; or abnormal
ceptor signalling, tissue development or synaptic transmission.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10;
                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid encoding Esel and 2 proteins, involved in regulation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     825 twqqksaftrtvspgsvspihgqgqavenl-----kaqalcswtakkenhinfskhdvi 878
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  endocytosis, used e.g. for treating cancer or preventing viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 21; Length 1197;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184 EVVEKSESGWWFCQMKAKRGWIPASFLEPLDSPD-ETEDPEPNYA-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 33; Page 48; 99pp; English.
                                                                                                                                                                                             Sengar A;
    98CA-2230201.
                                    99US-0118739
                                                                                                                                                                                                                                                                                                          N-PSDB; AAZ39010, AAZ39011
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                                                                                                                 (HSCR-) HSC RES & DEV LP.
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                                                                                                                                                                                                 Wang W,
                                    05-FEB-1999;
27-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                 Edan SE,
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EVVEKSESGWWFCQMKAKRGWIPASFLEPLDSPD-ETEDPEPNYA-
                                                                                                                                                                                                                                                                                    AAW05396
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proteins (1) and their splice variants (Ese = EH-domain and SH3-domain
regulator of endocytosis). (1) are involved in regulation of clathrin-
mediated endocytosis (as a complex with Esp15 protein), vesicular
trafficking and actin cytoskeleton. Generally (1) (or its (ant)agonists,
minetics, fragments and inactive mutents). (1) specific antibodies (Ab);
confices antisense to the (1) polyuncleotide; agents that downregulate
expression of Ese genes or antagonists of an Ese binding partner are
cused to treat diseases associated with undesirable endocytosis and
resulting changes in cellular function. Particularly overexpression of
Esel is used to block clathrin-mediated endocytosis in vivo or in cell
cultures, while administration of (1) is used to promote endocytosis of
selected cells. (Ant)agonists of (1) or Ab are used to suppress abnormal
proliferation of cells that can be stimulated to proliferate by a growth
cused to prevent viral infection. Endocytosis may also be regulated, in
vivo or in cell cultures, by forming an Ese-Esp15 complex, then binding
dynamin to the complex. Generally conditions that can be treated include
cancer; abnormal cell division or migration; viral infection; or abnormal
receptor signalling, tissue development or synaptic transmission. The
present sequence represents mouse Esell protein sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid encoding Esel and 2 proteins, involved in regulation of endocytosis, used e.g. for treating cancer or preventing viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              twqqksaftrtvspgsvspihgqgqavenl----kaqalcswtakkenhlnfskhdvi 878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80 WF-----DGQRAAENRQGTLTEYCSTLMSLPTKISRCP-HLLDFFKVRPDDLKLPT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130 DNQTKKPET-----YLMPKDGKSTATDITGPIILQTYRAIANYEKTSGSEMALSTGDVV 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           767 wfpcnyvekvlssekalspkkallpptvs--lsatstssqppasvtdyhnvsfsnltvnt 824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 21; Length 1658;
                                                                                                                                    Mouse; murine; Esel; Esel; endocytosis; vesicular trafficking; regulation; actin cytoskeleton; detection; cancer; infection; EH-domain and SH3-domain regulator of endocytosis; anticancer; antiproliferative; antiviral.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 33; Page 69-70; 99pp; English.
                                                                                                      Mouse Esell protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wang W, Sengar A;
                                                                                                                                                                                                                                                                                                                                                                    99WO-CA00375.
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99US-0118739.
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                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HSCR-) HSC RES & DEV LP.
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                                                                                                                                                                                                                                                                                    W09955728-A2.
                                                                                                                                                                                                                                                                                                                                                                    27-APR-1999;
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                                                            28-FEB-2000
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Best Local S
                    AAY57450;
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ANW05386-W05403 represent novel human and mouse Src-homology region 3

(5H3) domain containing proteins that can be used in the method of the invention. SH3 domain containing proteins play a role in signalling and structural elements of cells. The method of the invention is for identifying polypeptides containing functional domains of interest (especially SH3 domains). The method comprises contacting a multivalent correcognition unit (RN) complex with a number of peptides and indentifying polypeptides having a selective binding affinity for the RU complex. The method is based on functional similarities and does not rely on sequence similarities. Prior methods only gave limited success for identifying proteins which contain an SH3 domain due to the minimal sequence homology among known SH3 proteins. It has been found that small peptide main compared to monomer RUS. Multivalent for a given functional domains that are similar to, but not identical in sequence to, the original target functional domain. The new method enables proteins having a common function to be identified. Identification of novel SH3 proteins will be useful for a better understanding of cell growth, malignancy, signal transduction processes, etc. New candidate drugs can be identified, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cellular signaling element; cellular structural element; malignancy; protein identification; functional domain; protein screening; cellular signal transduction process.
                      937
                                                                                                                                    Src-homology region 3 domain; human; mouse; SH3 domain; cell growth;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying polypeptide(s) having specific functional domain (esp. SH3 domain) - comprises detecting selective binding to recognition unit, regardless of sequence homology
----GEPYVAIKAYTAVEGDEVSLLEGEAVEVIHKLLDGWKDDV---TGYFPSMYLQKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sparks AB;
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                                                                                                                                                                                                                                                                                                                 998 dge--nfgnasksgasnkkpeiagvtsayaas 1027
                                                                                                                                                                                                                                             280 GQDVSQAQRQIKRGAPPRRSSIRNAHSIHQRS 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW05396 standard; Protein; 248
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95US-0417872.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human SH3P18 protein.
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                                                                                                                                                                       105 gasn-kkpeiagvtsa---yvasgsegislapgglililkkntsgwwggelgargkkrgk 160
(e.g. pharmacological activities) can be assessed the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid encoding Esel and 2 proteins, involved in regulation of endocytosis, used e.g. for treating cancer or preventing viral
                                                                                                                               45 lypyssvepgdltftegeeilvtqkdgewwtgsigdrsgifpsnyvkpkdgesfgsasks 104
                                                                                                                                                     148 TATDITGPIILQTYRAIANYEKTSGSEMALSTGDVVEVVEKSESGWWFCQMKAK-----R 202
                                                                                        Gaps
                                                                                                                                                                                                            GWIPASFLEPLDSPDETEDPEPNYAGEP - - - YVAIKAYTAVEGDEVSLLEGEAVEVIHK -
                                                                                       47;
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                                                                  Length
                                                                                        68; Indels
                                                                                                            --PETYLMPKD-
                                                                DB 17;
                                                                8.7%; Score 176.5; DB 1
28.0%; Pred. No. 7.4e-09;
                                                                                     37; Mismatches
                                                                                                                                                                                                                                         259 LLDGWKDD---VTGYFPSMYLQ-KSGQDVSQ 285
                                                                                                                                                                                                                                                     AAY57444 standard; Protein; 1214 AA
                                                                                                           114 LLDFFKVRPDDLKLPTDNQ---TKK----
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                                                                                                                                                                                                                                                                                                                                                                                  Mouse Esel protein sequence
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N-PSDB; AAZ39008, AAZ39009.
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                                                                                     Conservative
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  their specificities using the method of
                                                                           Similarity
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                                 248 AA;
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Best Local Simi
Matches 59;
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polynucleotide; agents that downregulate expression of Ese genes or antagonists of an Ese binding partner are used to treat diseases associated with undesirable endocytosis and resulting changes in cellular function. Particularly overexpression of Esel is used to block clathrin-mediated endocytosis in vivo or in cell cultures, while administration of (I) is used to promote endocytosis of selected cells. (Ant)agonists of (I) or Ab are used to suppress abnormal proliferation of cells that can be stimulated to proliferate by a growth factor receptor; and similar compounds (also inactive Ese mutants) can be used to prevent viral infection. Endocytosis may also be regulated, in vivo or in cell complex. Benerally conditions that can be treated include cancer; abnormal cell division or migration; viral infection; or abnormal receptor signalling, tissue development or synaptic transmission.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----sssnekpetdnwdtwaagpsltvpsagglrgrsaftpatatgsspspvlgggek 906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              256 IHKLLDGWK---DDVTGYFPSMYLQ-KSGQDVSQAQRQIKRGAPPRRSSIRNAHSIHQRS 311
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20.1%; Pred. No. 2.3e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1214 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 88; Conserv
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The present invention specifically describes mammalian Esel and 2

Crequiator of endocytosis). (1) are involved in regulation of clathrin-
crequiator of endocytosis). (1) are involved in regulation of clathrin-
cmediated endocytosis (as a complex with Espl5 protein), vesicular
cmediated endocytosis (as a complex with Espl5 protein), vesicular
cmediated endocytosis (as a complex with Espl5 protein), vesicular
cmediated endocytosis (as a complex with Espl5 protein), vesicular
cmediated endocytosis (ab);
cccc trafficking and actin cytoskeleton. Generally (1) (or its (ant)agonists,
ccc and inserior can antagonists of an Ese binding partner are
ccc used to treat diseases associated with undesirable endocytosis and
cresulting changes in cellular function. Particularly overexpression of
csel is used to block clathrin-mediated endocytosis in vivo or in cell
ccc sells. (Ant)agonists of (1) or Ab are used to suppress abnormal
ccc activers, while administration of (1) is used to promote endocytosis of
collurars, while administration of (1) or Ab are used to suppress abnormal
ccc activers creeptor; and similar compounds (also inactive Ese mutants) can be
cused to prevent viral infection. Endocytosis may also be regulated, in
cused to prevent viral infection. Endocytosis may also be regulated, in
cused to complex. Generally conditions that can be treated include
cancer; abnormal cell division or migration; viral infection; or abnormal
cccpetor signalling, tissue development or synaptic transmission. The
cccpetor sequence represents mouse Esell protein sequence.
                                                                                                                                                                                                                                                                                                                                                          New nucleic acid encoding Esel and 2 proteins, involved in regulation of endocytosis, used e.g. for treating cancer or preventing viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 14; Page 62-63; 99pp; English.
                                                                                                                                                                                                                                          Wang W, Sengar A;
                                                                       99WO-CA00375
                                                                                                                 98CA-2230201.
                                                                                                                                                                                                                                                                                  WPI; 2000-052802/04.
N-PSDB; AAZ39024, AAZ39025.
                                                                                                                                                                                         (HSCR-) HSC RES & DEV LP.
                                                                     27-APR-1999;
                                                                                                                 27-APR-1998;
05-FEB-1999;
                      04-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                         infection
                                                                                                                                                                                                                                     Egan SE,
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27; Gaps Query Match
8.3%; Score 168.5; DB 21; Length 1715;
Best Local Similarity 31.2%; Pred. No. 8.6e-07;
Matches 54; Conservative 34; Mismatches 58; Indels 27;

1715 AA;

Sequence

11;

136 PETYLMPKDGKSTAT-DITG-----PIILQTYRAIANYEKTSGSEMALSTGDVVEVVEKS 189 οy g

190 ESGWWFCQMKA---KR--GWIPASFLEPLDSPDE---TEDPEPNYAGEP----YVAIKAY 237

δλ q ολ

Search completed: January 11, 2002, 09:08:48 Job time: 174 sec